

## SEQUENCE LISTING

<110> Chang, Chawnshang

<120> Androgen Receptor Coactivators

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<150> US 60/100,243

<151> 1998-09-14

<160> 147

-<170> PatentIn Ver. 2.0

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<223> Coding sequence and polypeptide region for the  
C-terminal domain.

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<222> (697)..(834)

<223> Coding sequence and polypeptide region which may  
form a cystein-rich RING finger motif.

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<222> (964)..(1089)

<223> Coding sequence and polypeptide region for a  
cystein-rich B box like structure.

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Arg Glu Ala Gln Glu Asp Glu Leu Leu Ala Leu Ala Ser Ile Tyr Asp
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gga gat gaa ttt aga aaa gca gag tct gtc caa ggt gga gaa acc agg      150
Gly Asp Glu Phe Arg Lys Ala Glu Ser Val Gln Gly Gly Glu Thr Arg
              25              30              35

atc tat ttg gat ttg cca cag aat ttc aag ata ttt gtg agc ggc aat      198
Ile Tyr Leu Asp Leu Pro Gln Asn Phe Lys Ile Phe Val Ser Gly Asn
              40              45              50

tca aat gag tgt ctc cag aat agt ggc ttt gaa tac acc att tgc ttt      246
Ser Asn Glu Cys Leu Gln Asn Ser Gly Phe Glu Tyr Thr Ile Cys Phe
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ctg cct cca ctt gtg ctg aac ttt gaa ctg cca cca gat tat cca tcc      294
Leu Pro Pro Leu Val Leu Asn Phe Glu Leu Pro Pro Asp Tyr Pro Ser
              70              75              80              85

tct tcc cca cct tca ttc aca ctt agt ggc aaa tgg ctg tca cca act      342
Ser Ser Pro Pro Ser Phe Thr Leu Ser Gly Lys Trp Leu Ser Pro Thr
              90              95              100

cag cta tct gct cta tgc aag cac tta gac aac cta tgg gaa gaa cac      390
Gln Leu Ser Ala Leu Cys Lys His Leu Asp Asn Leu Trp Glu Glu His
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cgt ggc agc gtg gtc ctg ttt gcc tgg atg caa ttt ctt aag gaa gag      438
Arg Gly Ser Val Val Leu Phe Ala Trp Met Gln Phe Leu Lys Glu Glu
              120              125              130

acc cta gca tac ttg aat att gtc tct cct ttt gag ctc aag att ggt      486
Thr Leu Ala Tyr Leu Asn Ile Val Ser Pro Phe Glu Leu Lys Ile Gly
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tct cag aaa aaa gtg cag aga agg aca gct caa gct tct ccc aac aca      534
Ser Gln Lys Lys Val Gln Arg Arg Thr Ala Gln Ala Ser Pro Asn Thr
              150              155              160              165

gag cta gat ttt gga gga gct gct gga tct gat gta gac caa gag gaa      582
Glu Leu Asp Phe Gly Gly Ala Ala Gly Ser Asp Val Asp Gln Glu Glu
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aat agt aaa ttg ttc ctg tgc agt atc tgt ttc tgt gag aag ctg ggt	726
Asn Ser Lys Leu Phe Leu Cys Ser Ile Cys Phe Cys Glu Lys Leu Gly	
215 220 225	
agt gaa tgc atg tac ttc ttg gag tgc agg cat gtg tac tgc aaa gcc	774
Ser Glu Cys Met Tyr Phe Leu Glu Cys Arg His Val Tyr Cys Lys Ala	
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Cys Leu Lys Asp Tyr Phe Glu Ile Gln Ile Arg Asp Gly Gln Val Gln	
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Cys Leu Asn Cys Pro Glu Pro Lys Cys Pro Ser Val Ala Thr Pro Gly	
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Gln Val Lys Glu Leu Val Glu Ala Glu Leu Phe Ala Arg Tyr Asp Arg	
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ctt ctc ctc cag tcc tcc ttg gac ctg atg gca gat gtg gtg tac tgc	966
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295 300 305	
ccc cgg ccg tgc tgc cag ctg cct gtg atg cag gaa cct ggc tgc acc	1014
Pro Arg Pro Cys Cys Gln Leu Pro Val Met Gln Glu Pro Gly Cys Thr	
310 315 320 325	
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Met Gly Ile Cys Ser Ser Cys Asn Phe Ala Phe Cys Thr Leu Cys Arg	
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ttg acc tac cat ggg gtc tcc cca tgt aag gtg act gca gag aaa tta	1110
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345 350 355	
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ctt ttg gat caa agg tat ggt aag aga gtg att cag aag gca ctg gaa	1206
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375 380 385	

gag atg gaa agt aag gag tgg cta gag aag aac tca aag agc tgc cca 1254  
 Glu Met Glu Ser Lys Glu Trp Leu Glu Lys Asn Ser Lys Ser Cys Pro  
 390 395 400 405

tgt tgt gga act ccc ata gag aaa tta gac gga tgt aac aag atg aca 1302  
 Cys Cys Gly Thr Pro Ile Glu Lys Leu Asp Gly Cys Asn Lys Met Thr  
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 Cys Thr Gly Cys Met Gln Tyr Phe Cys Trp Ile Cys Met Gly Ser Leu  
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 Ser Arg Ala Asn Pro Tyr Lys His Phe Asn Asp Pro Gly Ser Pro Cys  
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gat gag gta gaa gac tag ttaactactg ctcaagatat ttaactactg 1494  
 Asp Glu Val Glu Asp  
 470 475

ctcaagatat ggaagtggat tgtttttccc taatcttccg tcaagtacac aaagtaactt 1554

tgcgggatat ttaggggtact attcattcac tcttcctgcg tagaagatat ggaagaacga 1614

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Gly Gly Glu Thr Arg Ile Tyr Leu Asp Leu Pro Gln Asn Phe Lys Ile  
 35 40 45

Phe Val Ser Gly Asn Ser Asn Glu Cys Leu Gln Asn Ser Gly Phe Glu  
 50 55 60



Tyr Thr Ile Cys Phe Leu Pro Pro Leu Val Leu Asn Phe Glu Leu Pro  
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 Pro Asp Tyr Pro Ser Ser Ser Pro Pro Ser Phe Thr Leu Ser Gly Lys  
 85 90 95  
 Trp Leu Ser Pro Thr Gln Leu Ser Ala Leu Cys Lys His Leu Asp Asn  
 100 105 110  
 Leu Trp Glu Glu His Arg Gly Ser Val Val Leu Phe Ala Trp Met Gln  
 115 120 125  
 Phe Leu Lys Glu Glu Thr Leu Ala Tyr Leu Asn Ile Val Ser Pro Phe  
 130 135 140  
 Glu Leu Lys Ile Gly Ser Gln Lys Lys Val Gln Arg Arg Thr Ala Gln  
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 Ala Ser Pro Asn Thr Glu Leu Asp Phe Gly Gly Ala Ala Gly Ser Asp  
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 Val Asp Gln Glu Glu Ile Val Asp Glu Arg Ala Val Gln Asp Val Glu  
 180 185 190  
 Ser Leu Ser Asn Leu Ile Gln Glu Ile Leu Asp Phe Asp Gln Ala Gln  
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 Gln Ile Lys Cys Phe Asn Ser Lys Leu Phe Leu Cys Ser Ile Cys Phe  
 210 215 220  
 Cys Glu Lys Leu Gly Ser Glu Cys Met Tyr Phe Leu Glu Cys Arg His  
 225 230 235 240  
 Val Tyr Cys Lys Ala Cys Leu Lys Asp Tyr Phe Glu Ile Gln Ile Arg  
 245 250 255  
 Asp Gly Gln Val Gln Cys Leu Asn Cys Pro Glu Pro Lys Cys Pro Ser  
 260 265 270  
 Val Ala Thr Pro Gly Gln Val Lys Glu Leu Val Glu Ala Glu Leu Phe  
 275 280 285  
 Ala Arg Tyr Asp Arg Leu Leu Leu Gln Ser Ser Leu Asp Leu Met Ala  
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 Asp Val Val Tyr Cys Pro Arg Pro Cys Cys Gln Leu Pro Val Met Gln  
 305 310 315 320  
 Glu Pro Gly Cys Thr Met Gly Ile Cys Ser Ser Cys Asn Phe Ala Phe  
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Cys Thr Leu Cys Arg Leu Thr Tyr His Gly Val Ser Pro Cys Lys Val  
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Thr Ala Glu Lys Leu Met Asp Leu Arg Asn Glu Tyr Leu Gln Ala Asp  
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Glu Ala Asn Lys Arg Leu Leu Asp Gln Arg Tyr Gly Lys Arg Val Ile  
 370 375 380

Gln Lys Ala Leu Glu Glu Met Glu Ser Lys Glu Trp Leu Glu Lys Asn  
 385 390 395 400

Ser Lys Ser Cys Pro Cys Cys Gly Thr Pro Ile Glu Lys Leu Asp Gly  
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Cys Asn Lys Met Thr Cys Thr Gly Cys Met Gln Tyr Phe Cys Trp Ile  
 420 425 430

Cys Met Gly Ser Leu Ser Arg Ala Asn Pro Tyr Lys His Phe Asn Asp  
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tca gga gcc tcg ggg gac aag gac cac ctg tac agc acg gta tgc aag	144
Ser Gly Ala Ser Gly Asp Lys Asp His Leu Tyr Ser Thr Val Cys Lys	
35 40 45	
cct cgg tcc cca aag cct gca gcc ccg gcc gcc cct cca ttc tcc tct	192
Pro Arg Ser Pro Lys Pro Ala Ala Pro Ala Ala Pro Pro Phe Ser Ser	
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tcc agc ggt gtc ttg ggt acc ggg ctc tgt gag cta gat cgg ttg ctt	240
Ser Ser Gly Val Leu Gly Thr Gly Leu Cys Glu Leu Asp Arg Leu Leu	
65 70 75 80	
cag gaa ctt aat gcc act cag ttc aac atc aca gat gaa atc atg tct	288
Gln Glu Leu Asn Ala Thr Gln Phe Asn Ile Thr Asp Glu Ile Met Ser	
85 90 95	
cag ttc cca tct agc aag gtg gct tca gga gag cag aag gag gac cag	336
Gln Phe Pro Ser Ser Lys Val Ala Ser Gly Glu Gln Lys Glu Asp Gln	
100 105 110	
tct gaa gat aag aaa aga ccc agc ctc cct tcc agc ccg tct cct ggc	384
Ser Glu Asp Lys Lys Arg Pro Ser Leu Pro Ser Ser Pro Ser Pro Gly	
115 120 125	

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Leu Pro Lys Ala Ser Ala Thr Ser Ala Thr Leu Glu Leu Asp Arg Leu
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Met Ala Ser Leu Pro Asp Phe Arg Val Gln Asn His Leu Pro Ala Ser
145 150 155 160

ggg cca act cag cca ccg gtg gtg agc tcc aca aat gag ggc tcc cca 528
Gly Pro Thr Gln Pro Pro Val Val Ser Ser Thr Asn Glu Gly Ser Pro
165 170 175

tcc cca cca gag ccg act gca aag ggc agc cta gac acc atg ctg ggg 576
Ser Pro Pro Glu Pro Thr Ala Lys Gly Ser Leu Asp Thr Met Leu Gly
180 185 190

ctg ctg cag tcc gac ctc agc cgc cgg ggt gtt ccc acc cag gcc aaa 624
Leu Leu Gln Ser Asp Leu Ser Arg Arg Gly Val Pro Thr Gln Ala Lys
195 200 205

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Gly Leu Cys Gly Ser Cys Asn Lys Pro Ile Ala Gly Gln Val Val Thr
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gct ctg ggc cgc gcc tgg cac ccc gag cac ttc gtt tgc gga ggc tgt 720
Ala Leu Gly Arg Ala Trp His Pro Glu His Phe Val Cys Gly Gly Cys
225 230 235 240

tcc acc gcc ctg gga ggc agc agc ttc ttc gag aag gat gga gcc ccc 768
Ser Thr Ala Leu Gly Gly Ser Ser Phe Phe Glu Lys Asp Gly Ala Pro
245 250 255

ttc tgc ccc gag tgc tac ttt gag cgc ttc tgc cca aga tgt ggc ttc 816
Phe Cys Pro Glu Cys Tyr Phe Glu Arg Phe Ser Pro Arg Cys Gly Phe
260 265 270

tgc aac cag ccc atc cga cac aag atg gtg acc gcc ttg ggc act cac 864
Cys Asn Gln Pro Ile Arg His Lys Met Val Thr Ala Leu Gly Thr His
275 280 285

tgg cac cca gag cat ttc tgc tgc gtc agt tgc ggg gag ccc ttc gga 912
Trp His Pro Glu His Phe Cys Cys Val Ser Cys Gly Glu Pro Phe Gly
290 295 300

gat gag ggt ttc cac gag cgc gag ggc cgc ccc tac tgc cgc cgg gac 960
Asp Glu Gly Phe His Glu Arg Glu Gly Arg Pro Tyr Cys Arg Arg Asp
305 310 315 320

ttc ctg cag ctg ttc gcc ccg cgc tgc cag ggc tgc cag ggc ccc atc 1008
Phe Leu Gln Leu Phe Ala Pro Arg Cys Gln Gly Cys Gln Gly Pro Ile
325 330 335

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ctg gat aac tac atc tcg gcg ctc agc ctg ctc tgg cac ccg gac tgt 1056  
 Leu Asp Asn Tyr Ile Ser Ala Leu Ser Leu Leu Trp His Pro Asp Cys  
                   340                                  345                                  350

ttc gtc tgc agg gaa tgc ttc gcg ccc ttc tcg gga ggc agc ttt ttc 1104  
 Phe Val Cys Arg Glu Cys Phe Ala Pro Phe Ser Gly Gly Ser Phe Phe  
                   355                                  360                                  365

gag cac gag ggc cgc ccg ttg tgc gag aac cac ttc cac gca cga cgc 1152  
 Glu His Glu Gly Arg Pro Leu Cys Glu Asn His Phe His Ala Arg Arg  
                   370                                  375                                  380

ggc tcg ctg tgc ccc acg tgt ggc ctc cct gtg acc ggc cgc tgc gtg 1200  
 Gly Ser Leu Cys Pro Thr Cys Gly Leu Pro Val Thr Gly Arg Cys Val  
                   385                                  390                                  395                                  400

tcg gcc ctg ggt cgc cgc ttc cac ccg gac cac ttc gca tgc acc ttc 1248  
 Ser Ala Leu Gly Arg Arg Phe His Pro Asp His Phe Ala Cys Thr Phe  
                                   405                                  410                                  415

tgc ctg cgc ccg ctc acc aag ggg tcc ttc cag gag cgc gcc ggc aag 1296  
 Cys Leu Arg Pro Leu Thr Lys Gly Ser Phe Gln Glu Arg Ala Gly Lys  
                   420                                  425                                  430

ccc tac tgc cag ccc tgc ttc ctg aag ctc ttc ggc tga 1335  
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                   20                                  25                                  30

Ser Gly Ala Ser Gly Asp Lys Asp His Leu Tyr Ser Thr Val Cys Lys  
                   35                                  40                                  45

Pro Arg Ser Pro Lys Pro Ala Ala Pro Ala Ala Pro Pro Phe Ser Ser  
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Ser Ser Gly Val Leu Gly Thr Gly Leu Cys Glu Leu Asp Arg Leu Leu  
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Gln Glu Leu Asn Ala Thr Gln Phe Asn Ile Thr Asp Glu Ile Met Ser  
                   85                                  90                                  95

Gln Phe Pro Ser Ser Lys Val Ala Ser Gly Glu Gln Lys Glu Asp Gln  
 100 105 110  
 Ser Glu Asp Lys Lys Arg Pro Ser Leu Pro Ser Ser Pro Ser Pro Gly  
 115 120 125  
 Leu Pro Lys Ala Ser Ala Thr Ser Ala Thr Leu Glu Leu Asp Arg Leu  
 130 135 140  
 Met Ala Ser Leu Pro Asp Phe Arg Val Gln Asn His Leu Pro Ala Ser  
 145 150 155 160  
 Gly Pro Thr Gln Pro Pro Val Val Ser Ser Thr Asn Glu Gly Ser Pro  
 165 170 175  
 Ser Pro Pro Glu Pro Thr Ala Lys Gly Ser Leu Asp Thr Met Leu Gly  
 180 185 190  
 Leu Leu Gln Ser Asp Leu Ser Arg Arg Gly Val Pro Thr Gln Ala Lys  
 195 200 205  
 Gly Leu Cys Gly Ser Cys Asn Lys Pro Ile Ala Gly Gln Val Val Thr  
 210 215 220  
 Ala Leu Gly Arg Ala Trp His Pro Glu His Phe Val Cys Gly Gly Cys  
 225 230 235 240  
 Ser Thr Ala Leu Gly Gly Ser Ser Phe Phe Glu Lys Asp Gly Ala Pro  
 245 250 255  
 Phe Cys Pro Glu Cys Tyr Phe Glu Arg Phe Ser Pro Arg Cys Gly Phe  
 260 265 270  
 Cys Asn Gln Pro Ile Arg His Lys Met Val Thr Ala Leu Gly Thr His  
 275 280 285  
 Trp His Pro Glu His Phe Cys Cys Val Ser Cys Gly Glu Pro Phe Gly  
 290 295 300  
 Asp Glu Gly Phe His Glu Arg Glu Gly Arg Pro Tyr Cys Arg Arg Asp  
 305 310 315 320  
 Phe Leu Gln Leu Phe Ala Pro Arg Cys Gln Gly Cys Gln Gly Pro Ile  
 325 330 335  
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 340 345 350  
 Phe Val Cys Arg Glu Cys Phe Ala Pro Phe Ser Gly Gly Ser Phe Phe  
 355 360 365

Glu His Glu Gly Arg Pro Leu Cys Glu Asn His Phe His Ala Arg Arg  
 370 375 380

Gly Ser Leu Cys Pro Thr Cys Gly Leu Pro Val Thr Gly Arg Cys Val  
 385 390 395 400

Ser Ala Leu Gly Arg Arg Phe His Pro Asp His Phe Ala Cys Thr Phe  
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 Gln Phe Lys Leu Val Leu Val Gly Asp Gly Gly Thr Gly Lys Thr Thr  
 10 15 20 25

ttc gtg aaa cgt cat ttg act ggt gaa ttt gag aag aag tat gta gcc 147  
 Phe Val Lys Arg His Leu Thr Gly Glu Phe Glu Lys Lys Tyr Val Ala  
 30 35 40

acc ttg ggt gtt gag gtt cat ccc cta gtg ttc cac acc aac aga gga 195  
 Thr Leu Gly Val Glu Val His Pro Leu Val Phe His Thr Asn Arg Gly  
 45 50 55

cct att aag ttc aat gta tgg gac aca gcc ggc cag gag aaa ttc ggt 243  
 Pro Ile Lys Phe Asn Val Trp Asp Thr Ala Gly Gln Glu Lys Phe Gly  
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gga ctg aga gat ggc tat tat atc caa gcc cag tgt gcc atc ata atg 291  
 Gly Leu Arg Asp Gly Tyr Tyr Ile Gln Ala Gln Cys Ala Ile Ile Met  
 75 80 85

ttt gat gta aca tcg aga gtt act tac aag aat gtg cct aac tgg cat 339  
 Phe Asp Val Thr Ser Arg Val Thr Tyr Lys Asn Val Pro Asn Trp His  
 90 95 100 105

aga gat ctg gta cga gtg tgt gaa aac atc ccc att gtg ttg tgt ggc 387  
 Arg Asp Leu Val Arg Val Cys Glu Asn Ile Pro Ile Val Leu Cys Gly  
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aac aaa gtg gat att aag gac agg aaa gtg aag gcg aaa tcc att gtc 435  
 Asn Lys Val Asp Ile Lys Asp Arg Lys Val Lys Ala Lys Ser Ile Val  
 125 130 135

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 Phe His Arg Lys Lys Asn Leu Gln Tyr Tyr Asp Ile Ser Ala Lys Ser  
 140 145 150

aac tac aac ttt gaa aag ccc ttc ctc tgg ctt gct agg aag ctc att 531  
 Asn Tyr Asn Phe Glu Lys Pro Phe Leu Trp Leu Ala Arg Lys Leu Ile  
 155 160 165

gga gac cct aac ttg gaa ttt gtt gcc atg cct gct ctc gcc cca cca 579  
 Gly Asp Pro Asn Leu Glu Phe Val Ala Met Pro Ala Leu Ala Pro Pro  
 170 175 180 185

gaa gtt gtc atg gac cca gct ttg gca gca cag tat gag cac gac tta 627  
 Glu Val Val Met Asp Pro Ala Leu Ala Ala Gln Tyr Glu His Asp Leu  
 190 195 200

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 Glu Val Ala Gln Thr Thr Ala Leu Pro Asp Glu Asp Asp Asp Leu  
 205 210 215

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&lt;210&gt; 6

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&lt;213&gt; Homo sapien

&lt;400&gt; 6

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1				5				10					15		
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			20					25					30		
Gly	Glu	Phe	Glu	Lys	Lys	Tyr	Val	Ala	Thr	Leu	Gly	Val	Glu	Val	His
			35				40					45			
Pro	Leu	Val	Phe	His	Thr	Asn	Arg	Gly	Pro	Ile	Lys	Phe	Asn	Val	Trp
		50				55					60				
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Phe Leu Trp Leu Ala Arg Lys Leu Ile Gly Asp Pro Asn Leu Glu Phe  
 165 170 175

Val Ala Met Pro Ala Leu Ala Pro Pro Glu Val Val Met Asp Pro Ala  
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 Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala  
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acc gcc gcc gct gcc gcc gcg gaa ccc ccg gca ccg ccg ccg ccg ccc 218  
 Thr Ala Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro  
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cct cct gag gag gac cca gag cag gac agc ggc ccg gag gac ctg cct 266  
 Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro  
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ctc gtc agg ctt gag ttt gaa gaa aca gaa gaa cct gat ttt act gca 314  
 Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala  
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Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala	
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Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn	
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Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp	
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Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu	
160 165 170	
ata tat ttg aca caa ccc agc agt tcg ata tct act gaa ata aat tct	698
Ile Tyr Leu Thr Gln Pro Ser Ser Ile Ser Thr Glu Ile Asn Ser	
175 180 185	
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Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly	
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Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met	
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Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu	
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320 325 330	
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335 340 345	
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415 420 425	
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Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser	
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Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser	
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Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu	
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Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu	
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Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His	
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Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp	
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Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu	
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Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala	
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Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu	
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Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu	
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Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu	
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Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg	
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cca tat aaa att tca gaa ggt ctg cca aca cca aca aaa atg act cca	2618
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Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr	
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 Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys  
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 Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys  
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 Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp Glu  
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 Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val  
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His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val  
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 Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln  
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 Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys  
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 Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met  
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 Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys  
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 Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly  
 245 250 255  
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 Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val  
 275 280 285  
 Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly  
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 340 345 350  
 Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Val  
 355 360 365  
 Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln  
 370 375 380  
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Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu  
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 Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys  
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 Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu  
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 Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu  
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 485 490 495  
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 580 585 590  
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 Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser  
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 625 630 635 640  
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His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu  
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Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met  
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Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys  
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Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln  
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Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile  
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Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile  
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Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His  
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Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro  
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Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser  
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Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu  
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Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile  
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Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu  
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Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu  
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Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys  
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 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
       synthetic construct

<400> 13  
 ctgcagcttg ttctttaatg tcaggagact ctcccttctg cttgtcctgg tgggccctgg 60  
 ggggagcggg gaggaatac ctaagagcaa ttggtagctg gtacttctaa tgcctcttcc 120  
 tcctccaacc tccaagagtc tgttttggga ttgggttcag gaatgaaatt ctgcctgtgc 180  
 taacctcctg gggagccggt agacttgtct gttaaaaatc gcttctgctt ttggagccta 240  
 aagcccggtt ccgaaaaaca agtggtatct aggggaaaga ggggtcttca aaggctacag 300  
 tgagtcattc cagccttcaa ccatactacg ccagcactac gttctctaaa gccactctgc 360  
 gctagcttgc ggtgagggga ggggagaaaa ggaaagggga ggggagggga ggggagggag 420  
 aaaggaggtg ggaaggcaga gaggcgggct gcggggcgcg gaccgactca caaactgttc 480  
 gatttcggtt ccacctccca gcgccccctc ggagatccct aggagccagc ctgctgggag 540  
 aaccagaggg tccggagcaa acctggaggc tgagagggga tcagagggga aaagactgag 600  
 ctagccactc cagtgccata cagaagctta agggacgcac cacgccagcc ccagcccagc 660  
 gacagccaac gcctgttgca gagcggcggc ttcgaaagccg ccgcccagga gctgcccttt 720  
 cctcttcggt gaagtctcta aaagctgcgg gagactcaga ggaagcaagg aaagtgtccg 780  
 gtaggactac ggctgccttt gtctcttctc cctctacctt taccctctcc tgggtcccct 840  
 ctccaggagc tgactaggca ggctttcttg ccaacctctc cccctacacc cccagctctg 900  
 ccagccagtt tgcacagagg taaactccct ttggctgaga gtaggggagc ttgttgca 960  
 ttgcaaggaa ggcttttggt agcccagaga ctgaggagca acagcacgcc caggagagtc 1020  
 cctggttcca ggttctcgcc cctgcacctc ctctgcccg cccctcacc cgtgtgtggt 1080  
 gttagaaatg aaaagatgaa aaggcagcta ggggttcagt agtcgaaagc aaaacaaaag 1140  
 ctaaaagaaa acaaaaagaa aatagcccag ttcttatttg cacctgcttc agtggacttt 1200  
 gaatttgaaa ggcagaggat tccccctttt ccctcccgtc aagggttgag catcttttaa 1260  
 tctgttcttc aagtatttag agacaaaact tgtaagtagc agggcagatc ctgtcttgcg 1320  
 cgtgccttcc tttactggag actttgaggt tatctgggca ctccccccac ccaccccccc 1380  
 tcctgcaagt tttcttcccc ggagcttccc gcaggtgggc agctagctgc agatactaca 1440  
 tcatacgtca ggagaactct tcagagcaag agacgaggag gcaggataag ggaattc 1497

<210> 14  
 <211> 600  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
       synthetic construct

<400> 14  
 ctgcagcttg ttctttaatg tcaggagact ctcccttctg cttgtcctgg tgggccctgg 60  
 ggggagcggg gaggaatac ctaagagcaa ttggtagctg gtacttctaa tgcctcttcc 120  
 tcctccaacc tccaagagtc tgttttggga ttgggttcag gaatgaaatt ctgcctgtgc 180  
 taacctcctg gggagccggt agacttgtct gttaaaaatc gcttctgctt ttggagccta 240  
 aagcccggtt ccgaaaaaca agtggtatct aggggaaaga ggggtcttca aaggctacag 300  
 tgagtcattc cagccttcaa ccatactacg ccagcactac gttctctaaa gccactctgc 360  
 gctagcttgc ggtgagggga ggggagaaaa ggaaagggga ggggagggga ggggagggag 420

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aaaggaggtg ggaaggcaga gaggccggct gcgggggcgg gaccgactca caaactgttc      480
gatttcgttt ccacctccca gcgccccctc ggagatccct aggagccagc ctgctgggag      540
aaccagaggg tccggagcaa acctggaggc tgagagggga tcagagggga aaagactgag      600

```

&lt;210&gt; 15

&lt;211&gt; 359

&lt;212&gt; .DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 15

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cccaagcgct agtgttctgt tctctttttg taatcttga atcttttgtt gctctaaata      60
caattaaaaa tggcagaaac ttgtttgttg gaatacatgt gtgactcttg gtttgtctct      120
gcgtctggct ttagaaatgt catccattgt gtaaaatact ggcttggttg tctgccagct      180
aaaacttgcc acagcccctg ttgtgactgc aggctcaagt tattgttaac aaagagcccc      240
aagaaaagct gctaattgtc tcttatcacc attgttaatt tgttaaaaca taaaacaatc      300
taaaatttca gatgaatgtc atcagagttc ttttcattag ctctttttat tggctgtct      359

```

&lt;210&gt; 16

&lt;211&gt; 899

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 16

```

Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser
 1          5          10          15
Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
 20          25          30
Ala Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Asn Ile Ala
 35          40          45
Pro Pro Gly Ala Cys Leu Gln Gln Arg Gln Glu Thr Ser Pro Arg Arg
 50          55          60
Arg Arg Arg Gln Gln His Thr Glu Asp Gly Ser Pro Gln Ala His Ile
 65          70          75          80
Arg Gly Pro Thr Gly Tyr Leu Ala Leu Glu Glu Gln Gln Pro Ser
 85          90          95
Gln Gln Gln Ala Ala Ser Glu Gly His Pro Glu Ser Ser Cys Leu Pro
100          105          110
Glu Pro Gly Ala Ala Thr Ala Pro Gly Lys Gly Leu Pro Gln Gln Pro
115          120          125
Pro Ala Pro Pro Asp Gln Asp Asp Ser Ala Ala Pro Ser Thr Leu Ser
130          135          140
Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser Ala Asp Ile
145          150          155          160
Lys Asp Ile Leu Asn Glu Ala Gly Thr Met Gln Leu Leu Gln Gln Gln
165          170          175
Gln Gln Gln Gln Gln His Gln Gln Gln His Gln Gln His Gln Gln Gln
180          185          190
Gln Glu Val Ile Ser Glu Gly Ser Ser Ala Arg Ala Arg Glu Ala Thr
195          200          205
Gly Ala Pro Ser Ser Ser Lys Asp Ser Tyr Leu Gly Gly Asn Ser Thr
210          215          220
Ile Ser Asp Ser Ala Lys Glu Leu Cys Lys Ala Val Ser Val Ser Met
225          230          235          240

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Gly	Leu	Gly	Val	Glu	Ala	Leu	Glu	His	Leu	Ser	Pro	Gly	Glu	Gln	Leu	245	250	255
Arg	Gly	Asp	Cys	Met	Tyr	Ala	Ser	Leu	Leu	Gly	Gly	Pro	Pro	Ala	Val	260	265	270
Arg	Pro	Thr	Pro	Cys	Ala	Pro	Leu	Pro	Glu	Cys	Lys	Gly	Leu	Pro	Leu	275	280	285
Asp	Glu	Gly	Pro	Gly	Lys	Ser	Thr	Glu	Glu	Thr	Ala	Glu	Tyr	Ser	Ser	290	295	300
Phe	Lys	Gly	Gly	Tyr	Ala	Lys	Gly	Leu	Glu	Gly	Glu	Ser	Leu	Gly	Cys	305	310	315
Ser	Gly	Ser	Ser	Glu	Ala	Gly	Ser	Ser	Gly	Thr	Leu	Glu	Ile	Pro	Ser	325	330	335
Ser	Leu	Ser	Leu	Tyr	Lys	Ser	Gly	Ala	Leu	Asp	Glu	Ala	Ala	Ala	Tyr	340	345	350
Gln	Asn	Arg	Asp	Tyr	Tyr	Asn	Phe	Pro	Leu	Ala	Leu	Ser	Gly	Pro	Pro	355	360	365
His	Pro	Pro	Pro	Pro	Thr	His	Pro	His	Ala	Arg	Ile	Lys	Leu	Glu	Asn	370	375	380
Pro	Leu	Asp	Tyr	Gly	Ser	Ala	Trp	Ala	Ala	Ala	Ala	Ala	Gln	Cys	Arg	385	390	395
Tyr	Gly	Asp	Leu	Gly	Ser	Leu	His	Gly	Gly	Ser	Val	Ala	Gly	Pro	Ser	405	410	415
Thr	Gly	Ser	Pro	Pro	Ala	Thr	Thr	Ser	Ser	Ser	Trp	His	Thr	Leu	Phe	420	425	430
Thr	Ala	Glu	Gly	Gln	Leu	Tyr	Gly	Pro	Gly	Gly	Gly	Gly	Gly	Gly	Ser	435	440	445
Ser	Ser	Pro	Ser	Asp	Ala	Gly	Pro	Val	Ala	Pro	Tyr	Gly	Tyr	Thr	Arg	450	455	460
Pro	Pro	Gln	Gly	Leu	Thr	Ser	Gln	Glu	Ser	Asp	Tyr	Ser	Ala	Ser	Glu	465	470	475
Val	Trp	Tyr	Pro	Gly	Gly	Val	Val	Asn	Arg	Val	Pro	Tyr	Pro	Ser	Pro	485	490	495
Asn	Cys	Val	Lys	Ser	Glu	Met	Gly	Pro	Trp	Met	Glu	Asn	Tyr	Ser	Gly	500	505	510
Pro	Tyr	Gly	Asp	Met	Arg	Leu	Asp	Ser	Thr	Arg	Asp	His	Val	Leu	Pro	515	520	525
Ile	Asp	Tyr	Tyr	Phe	Pro	Pro	Gln	Lys	Thr	Cys	Leu	Ile	Cys	Gly	Asp	530	535	540
Glu	Ala	Ser	Gly	Cys	His	Tyr	Gly	Ala	Leu	Thr	Cys	Gly	Ser	Cys	Lys	545	550	555
Val	Phe	Phe	Lys	Arg	Ala	Ala	Glu	Gly	Lys	Gln	Lys	Tyr	Leu	Cys	Ala	565	570	575
Ser	Arg	Asn	Asp	Cys	Thr	Ile	Asp	Lys	Phe	Arg	Arg	Lys	Asn	Cys	Pro	580	585	590
Ser	Cys	Arg	Leu	Arg	Lys	Cys	Tyr	Glu	Ala	Gly	Met	Thr	Leu	Gly	Ala	595	600	605
Arg	Lys	Leu	Lys	Lys	Leu	Gly	Asn	Leu	Lys	Leu	Gln	Glu	Glu	Gly	Glu	610	615	620
Asn	Ser	Asn	Ala	Gly	Ser	Pro	Thr	Glu	Asp	Pro	Ser	Gln	Lys	Met	Thr	625	630	635
Val	Ser	His	Ile	Glu	Gly	Tyr	Glu	Cys	Gln	Pro	Ile	Phe	Leu	Asn	Val	645	650	655
Leu	Glu	Ala	Ile	Glu	Pro	Gly	Val	Val	Cys	Ala	Gly	His	Asp	Asn	Asn	660	665	670
Gln	Pro	Asp	Ser	Phe	Ala	Ala	Leu	Leu	Ser	Ser	Leu	Asn	Glu	Leu	Gly	675	680	685
Glu	Arg	Gln	Leu	Val	His	Val	Val	Lys	Trp	Ala	Lys	Ala	Leu	Pro	Gly	690	695	700
Phe	Arg	Asn	Leu	His	Val	Asp	Asp	Gln	Met	Ala	Val	Ile	Gln	Tyr	Ser	705	710	715



Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser Phe Thr Asn  
 725 730 735  
 Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val Phe Asn Glu  
 740 745 750  
 Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val Arg Met Arg  
 755 760 765  
 His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro Gln Glu Phe  
 770 775 780  
 Leu Cys Met Lys Ala Leu Leu Phe Ser Ile Ile Pro Val Asp Gly  
 785 790 795 800  
 Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn Tyr Ile Lys  
 805 810 815  
 Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro Thr Ser Cys  
 820 825 830  
 Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln Pro  
 835 840 845  
 Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu Ile Lys Ser  
 850 855 860  
 His Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu Ile Ile Ser  
 865 870 875 880  
 Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr Phe  
 885 890 895  
 His Thr Gln

&lt;210&gt; 17

&lt;211&gt; 2988

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
 synthetic construct

&lt;400&gt; 17

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gagcaagaga	cgaggaggca	ggataaggga	attcgggtgga	agctacagac	aagctcaagg	120
atggagggtgc	agttagggct	gggaagggtc	taccacggc	ccccatccaa	gacctatcga	180
ggagcgttcc	agaatctgtt	ccagagcgtg	cgcgaaagcga	tccagaaccc	gggccccagg	240
caccctgagg	ccgctaacat	agcacctccc	ggcgctgtt	tacagcagag	gcaggagact	300
agcccccggc	ggcggcggcg	gcagcagcac	actgaggatg	gttctcctca	agccccacatc	360
agaggcccca	caggctacct	ggccctggag	gaggaacagc	agccttcaca	gcagcaggga	420
gcctccgagg	gccaccctga	gagcagctgc	ctccccgagc	ctggggcggc	caccgctcct	480
ggcaaggggc	tgccgcagca	gccaccagct	cctccagatc	aggatgactc	agctgccccca	540
tccacgttgt	ccctgctggg	ccccactttc	ccaggcttaa	gcagctgctc	cgccgacatt	600
aaagacattt	tgaacgaggc	cggcaccatg	caacttcttc	agcagcagca	acaacagcag	660
cagcaccaac	agcagcacca	acagcaccaa	cagcagcagg	aggtaatctc	cgaaggcagc	720
agcgcaagag	ccagggaggc	cacgggggct	ccctcttcc	ccaaggatag	ttacctaggg	780
ggcaattcaa	ccatatctga	cagtgcgaag	gagttgtgta	aagcagtgct	tgtgtccatg	840
ggattgggtg	tggaagcatt	ggaacatctg	agtccagggg	aacagcttcg	gggagactgc	900
atgtacgcgt	cgctcctggg	aggtccaccc	gcggtgcgtc	ccactccttg	tgcgcgctg	960
cccgaatgca	aaggctcttc	cctggacgaa	ggcccaggca	aaagcactga	agagactgct	1020
gagtatctct	ctttcaaggg	aggttacgcc	aaaggattgg	aaggtagagag	cttgggggtgc	1080
tctggcagca	gtgaagcagg	tagctctggg	acacttgaga	tcccgctctc	tctgtctctg	1140
tataaatctg	gagcactaga	cgaggcagca	gcataccaga	atcgcgacta	ctacaacttt	1200
ccgctggctc	tgtccggggc	gccgcacccc	ccgcccccta	cccatccaca	cgcccgatc	1260
aagctggaga	acccattgga	ctacggcagc	gcctgggctg	cggcggcagc	gcaatgccgc	1320
tatggggact	tgggtagtct	acatggaggg	agtgtagccg	ggcccagcac	tggatcgccc	1380
ccagccacca	cctcttcttc	ctggcatact	ctcttcacag	ctgaagaagg	ccaattatat	1440
gggccaggag	gcgggggcgg	cagcagcagc	ccaagcgatg	ccgggcctgt	agccccctat	1500
ggctacactc	ggccccctca	ggggctgaca	agccaggaga	gtgactactc	tgccctccgaa	1560

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gtgtggtatc ctggtggagt tgtgaacaga gtaccctatc ccagtcccaa ttgtgtcaaa 1620
agtgaatatg gaccttggtat ggagaactac tccggacctt atgggggacat gcgtttggac 1680
agtaccaggg accatgtttt acccatcgac tattactttc caccaccagaa gacctgcctg 1740
atctgtggag atgaagcttc tggctgtcac tacggagctc tcacttgtgg cagctgcaag 1800
gtcttcttca aaagagccgc tgaagggaaa cagaagtatc tatgtgccag cagaaacgat 1860
tgtaccattg ataaatttcg gaggaaaaaat tgcccatctt gtcgtctccg gaaatgttat 1920
gaagcaggga tgactctggg agctcgttaag ctgaagaaac ttggaaatct aaaactacag 1980
gaggaaggag aaaactccaa tgctggcagc cccactgagg acccatccca gaagatgact 2040
gtatcacaca ttgaaggcta tgaatgtcag cctatctttc ttaacgtcct ggaagccatt 2100
gagccaggag tgggtgtgtgc cggacatgac aacaaccaac cagattcctt tgctgccttg 2160
ttatctagcg tcaatgagct tggagagagg cagcttgtgc atgtgggtcaa gtggggccaa 2220
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tggatggggac tgatggtatt tgccatgggt tggcgggtcct tcactaatgt caactccagg 2340
atgctctact ttgcacctga cttgggttttc aatgagtacc gcatgcacaa gtctcggatg 2400
tacagccagt gtgtgaggat gaggcacctg tctcaagagt ttggatggct ccaaataacc 2460
ccccaggaat tcctgtgcat gaaagcactg ctgctcttca gcattattcc agtggatggg 2520
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atcattgcat gcaaaagaaa gaatcccaca tcctgctcaa ggcgcttcta ccagctcacc 2640
aagtccttgg attctgtgca gcctattgca agagagctgc atcagttcac ttttgacctg 2700
ctaatacagt cccatatggt gagcgtggac tttcctgaaa tgatggcaga gatcatctct 2760
gtgcaagtgc ccaagatcct ttctgggaaa gtcaagccca tctatttcca cacacagtga 2820
agatttggaa accctaatac ccaaaaccca ccttgttccc tttccagatg tcttctgcct 2880
gttatataac tctgcactac ttctctgcag tgccttgggg gaaattcctc tactgatgta 2940
cagtcagacg tgaacaggtt cctcagttct atttctctgg cttctcct 2988

```

&lt;210&gt; 18

&lt;211&gt; 899

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 18

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Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser
1          5          10          15
Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
20        25        30
Ala Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Asn Ile Ala
35        40        45
Pro Pro Gly Ala Cys Leu Gln Gln Arg Gln Glu Thr Ser Pro Arg Arg
50        55        60
Arg Arg Arg Gln Gln His Thr Glu Asp Gly Ser Pro Gln Ala His Ile
65        70        75        80
Arg Gly Pro Thr Gly Tyr Leu Ala Leu Glu Glu Glu Gln Gln Pro Ser
85        90        95
Gln Gln Gln Ala Ala Ser Glu Gly His Pro Glu Ser Ser Cys Leu Pro
100       105       110
Glu Pro Gly Ala Ala Thr Ala Pro Gly Lys Gly Leu Pro Gln Gln Pro
115       120       125
Pro Ala Pro Pro Asp Gln Asp Ser Ala Ala Pro Ser Thr Leu Ser
130       135       140
Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser Ala Asp Ile
145       150       155       160
Lys Asp Ile Leu Asn Glu Ala Gly Thr Met Gln Leu Leu Gln Gln Gln
165       170       175
Gln Gln Gln Gln Gln His Gln Gln Gln His Gln Gln Gln Gln Gln
180       185       190
Gln Glu Val Ile Ser Glu Gly Ser Ser Ala Arg Ala Arg Glu Ala Thr
195       200       205

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Gly	Ala	Pro	Ser	Ser	Ser	Lys	Asp	Ser	Tyr	Leu	Gly	Gly	Asn	Ser	Thr
210						215					220				
Ile	Ser	Asp	Ser	Ala	Lys	Glu	Leu	Cys	Lys	Ala	Val	Ser	Val	Ser	Met
225					230					235					240
Gly	Leu	Gly	Val	Glu	Ala	Leu	Glu	His	Leu	Ser	Pro	Gly	Glu	Gln	Leu
				245					250					255	
Arg	Gly	Asp	Cys	Met	Tyr	Ala	Ser	Leu	Leu	Gly	Gly	Pro	Pro	Ala	Val
			260					265						270	
Arg	Pro	Thr	Pro	Cys	Ala	Pro	Leu	Pro	Glu	Cys	Lys	Gly	Leu	Pro	Leu
		275					280					285			
Asp	Glu	Gly	Pro	Gly	Lys	Ser	Thr	Glu	Glu	Thr	Ala	Glu	Tyr	Ser	Ser
	290					295					300				
Phe	Lys	Gly	Gly	Tyr	Ala	Lys	Gly	Leu	Glu	Gly	Glu	Ser	Leu	Gly	Cys
305					310					315					320
Ser	Gly	Ser	Ser	Glu	Ala	Gly	Ser	Ser	Gly	Thr	Leu	Glu	Ile	Pro	Ser
				325					330					335	
Ser	Leu	Ser	Leu	Tyr	Lys	Ser	Gly	Ala	Leu	Asp	Glu	Ala	Ala	Ala	Tyr
			340					345					350		
Gln	Asn	Arg	Asp	Tyr	Tyr	Asn	Phe	Pro	Leu	Ala	Leu	Ser	Gly	Pro	Pro
		355					360					365			
His	Pro	Pro	Pro	Pro	Thr	His	Pro	His	Ala	Arg	Ile	Lys	Leu	Glu	Asn
	370				375						380				
Pro	Leu	Asp	Tyr	Gly	Ser	Ala	Trp	Ala	Ala	Ala	Ala	Ala	Gln	Cys	Arg
385					390					395					400
Tyr	Gly	Asp	Leu	Gly	Ser	Leu	His	Gly	Gly	Ser	Val	Ala	Gly	Pro	Ser
				405				410						415	
Thr	Gly	Ser	Pro	Pro	Ala	Thr	Thr	Ser	Ser	Ser	Trp	His	Thr	Leu	Phe
			420				425						430		
Thr	Ala	Glu	Glu	Gly	Gln	Leu	Tyr	Gly	Pro	Gly	Gly	Gly	Gly	Gly	Ser
		435					440				445				
Ser	Ser	Pro	Ser	Asp	Ala	Gly	Pro	Val	Ala	Pro	Tyr	Gly	Tyr	Thr	Arg
	450				455					460					
Pro	Pro	Gln	Gly	Leu	Thr	Ser	Gln	Glu	Ser	Asp	Tyr	Ser	Ala	Ser	Glu
465					470					475					480
Val	Trp	Tyr	Pro	Gly	Gly	Val	Val	Asn	Arg	Val	Pro	Tyr	Pro	Ser	Pro
				485				490						495	
Asn	Cys	Val	Lys	Ser	Glu	Met	Gly	Pro	Trp	Met	Glu	Asn	Tyr	Ser	Gly
			500				505						510		
Pro	Tyr	Gly	Asp	Met	Arg	Leu	Asp	Ser	Thr	Arg	Asp	His	Val	Leu	Pro
	515						520				525				
Ile	Asp	Tyr	Tyr	Phe	Pro	Pro	Gln	Lys	Thr	Cys	Leu	Ile	Cys	Gly	Asp
	530				535						540				
Glu	Ala	Ser	Gly	Cys	His	Tyr	Gly	Ala	Leu	Thr	Cys	Gly	Ser	Cys	Lys
				550						555					560
Val	Phe	Phe	Lys	Arg	Ala	Ala	Glu	Gly	Lys	Gln	Lys	Tyr	Leu	Cys	Ala
				565				570						575	
Ser	Arg	Asn	Asp	Cys	Thr	Ile	Asp	Lys	Phe	Arg	Arg	Lys	Asn	Cys	Pro
			580				585						590		
Ser	Cys	Arg	Leu	Arg	Lys	Cys	Tyr	Glu	Ala	Gly	Met	Thr	Leu	Gly	Ala
	595						600				605				
Arg	Lys	Leu	Lys	Lys	Leu	Gly	Asn	Leu	Lys	Leu	Gln	Glu	Glu	Gly	Glu
	610				615						620				
Asn	Ser	Asn	Ala	Gly	Ser	Pro	Thr	Glu	Asp	Pro	Ser	Gln	Lys	Met	Thr
625					630					635					640
Val	Ser	His	Ile	Glu	Gly	Tyr	Glu	Cys	Gln	Pro	Ile	Phe	Leu	Asn	Val
				645					650					655	
Leu	Glu	Ala	Ile	Glu	Pro	Gly	Val	Val	Cys	Ala	Gly	His	Asp	Asn	Asn
			660				665						670		
Gln	Pro	Asp	Ser	Phe	Ala	Ala	Leu	Leu	Ser	Ser	Leu	Asn	Glu	Leu	Gly
		675					680					685			

Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys Ala Leu Pro Gly  
 690 695 700  
 Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile Gln Tyr Ser  
 705 710 715 720  
 Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser Phe Thr Asn  
 725 730 735  
 Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val Phe Asn Glu  
 740 745 750  
 Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val Arg Met Arg  
 755 760 765  
 His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro Gln Glu Phe  
 770 775 780  
 Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro Val Asp Gly  
 785 790 795 800  
 Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn Tyr Ile Lys  
 805 810 815  
 Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro Thr Ser Cys  
 820 825 830  
 Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln Pro  
 835 840 845  
 Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu Ile Lys Ser  
 850 855 860  
 His Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu Ile Ile Ser  
 865 870 875 880  
 Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr Phe  
 885 890 895  
 His Thr Gln

&lt;210&gt; 19

&lt;211&gt; 2988

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
 synthetic construct

&lt;400&gt; 19

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&lt;210&gt; 20

&lt;211&gt; 899

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 20

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Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
 20          25          30
Ala Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Asn Ile Ala
 35          40          45
Pro Pro Gly Ala Cys Leu Gln Gln Arg Gln Glu Thr Ser Pro Arg Arg
 50          55          60
Arg Arg Arg Gln Gln His Thr Glu Asp Gly Ser Pro Gln Ala His Ile
 65          70          75          80
Arg Gly Pro Thr Gly Tyr Leu Ala Leu Glu Glu Gln Gln Pro Ser
 85          90          95
Gln Gln Gln Ala Ala Ser Glu Gly His Pro Glu Ser Ser Cys Leu Pro
100          105          110
Glu Pro Gly Ala Ala Thr Ala Pro Gly Lys Gly Leu Pro Gln Gln Pro
115          120          125
Pro Ala Pro Pro Asp Gln Asp Asp Ser Ala Ala Pro Ser Thr Leu Ser
130          135          140
Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser Ala Asp Ile
145          150          155          160

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Lys Asp Ile Leu Asn Glu Ala Gly Thr Met Gln Leu Leu Gln Gln Gln  
 165 170 175  
 Gln Gln Gln Gln Gln His Gln Gln Gln His Gln Gln His Gln Gln Gln  
 180 185 190  
 Gln Glu Val Ile Ser Glu Gly Ser Ser Ala Arg Ala Arg Glu Ala Thr  
 195 200 205  
 Gly Ala Pro Ser Ser Ser Lys Asp Ser Tyr Leu Gly Gly Asn Ser Thr  
 210 215 220  
 Ile Ser Asp Ser Ala Lys Glu Leu Cys Lys Ala Val Ser Val Ser Met  
 225 230 235 240  
 Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser Pro Gly Glu Gln Leu  
 245 250 255  
 Arg Gly Asp Cys Met Tyr Ala Ser Leu Leu Gly Gly Pro Pro Ala Val  
 260 265 270  
 Arg Pro Thr Pro Cys Ala Pro Leu Pro Glu Cys Lys Gly Leu Pro Leu  
 275 280 285  
 Asp Glu Gly Pro Gly Lys Ser Thr Glu Glu Thr Ala Glu Tyr Ser Ser  
 290 295 300  
 Phe Lys Gly Gly Tyr Ala Lys Gly Leu Glu Gly Glu Ser Leu Gly Cys  
 305 310 315 320  
 Ser Gly Ser Ser Glu Ala Gly Ser Ser Gly Thr Leu Glu Ile Pro Ser  
 325 330 335  
 Ser Leu Ser Leu Tyr Lys Ser Gly Ala Leu Asp Glu Ala Ala Tyr  
 340 345 350  
 Gln Asn Arg Asp Tyr Tyr Asn Phe Pro Leu Ala Leu Ser Gly Pro Pro  
 355 360 365  
 His Pro Pro Pro Pro Thr His Pro His Ala Arg Ile Lys Leu Glu Asn  
 370 375 380  
 Pro Leu Asp Tyr Gly Ser Ala Trp Ala Ala Ala Ala Gln Cys Arg  
 385 390 395 400  
 Tyr Gly Asp Leu Gly Ser Leu His Gly Gly Ser Val Ala Gly Pro Ser  
 405 410 415  
 Thr Gly Ser Pro Pro Ala Thr Thr Ser Ser Ser Trp His Thr Leu Phe  
 420 425 430  
 Thr Ala Glu Glu Gly Gln Leu Tyr Gly Pro Gly Gly Gly Gly Ser  
 435 440 445  
 Ser Ser Pro Ser Asp Ala Gly Pro Val Ala Pro Tyr Gly Tyr Thr Arg  
 450 455 460  
 Pro Pro Gln Gly Leu Thr Ser Gln Glu Ser Asp Tyr Ser Ala Ser Glu  
 465 470 475 480  
 Val Trp Tyr Pro Gly Gly Val Val Asn Arg Val Pro Tyr Pro Ser Pro  
 485 490 495  
 Asn Cys Val Lys Ser Glu Met Gly Pro Trp Met Glu Asn Tyr Ser Gly  
 500 505 510  
 Pro Tyr Gly Asp Met Arg Leu Asp Ser Thr Arg Asp His Val Leu Pro  
 515 520 525  
 Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys Leu Ile Cys Gly Asp  
 530 535 540  
 Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr Cys Gly Ser Cys Lys  
 545 550 555 560  
 Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys Tyr Leu Cys Ala  
 565 570 575  
 Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg Lys Asn Cys Pro  
 580 585 590  
 Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met Thr Leu Gly Ala  
 595 600 605  
 Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu Glu Gly Glu  
 610 615 620  
 Asn Ser Asn Ala Gly Ser Pro Thr Glu Asp Pro Ser Gln Lys Met Thr  
 625 630 635 640

Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe Leu Asn Val  
 645 650 655  
 Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His Asp Asn Asn  
 660 665 670  
 Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn Glu Leu Gly  
 675 680 685  
 Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys Ala Leu Pro Gly  
 690 695 700  
 Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile Gln Tyr Ser  
 705 710 715 720  
 Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser Phe Thr Asn  
 725 730 735  
 Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val Phe Asn Glu  
 740 745 750  
 Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val Arg Met Arg  
 755 760 765  
 His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro Gln Glu Phe  
 770 775 780  
 Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro Val Asp Gly  
 785 790 795 800  
 Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn Tyr Ile Lys  
 805 810 815  
 Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro Thr Ser Cys  
 820 825 830  
 Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln Pro  
 835 840 845  
 Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu Ile Lys Ser  
 850 855 860  
 His Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu Ile Ile Ser  
 865 870 875 880  
 Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr Phe  
 885 890 895  
 His Thr Gln

<210> 21

<211> 2700

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 21

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gcctccgagg	gccaccctga	gagcagctgc	ctccccgagc	ctggggcggc	caccgctcct	360
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cagcaccaac	agcagcacca	acagcaccaa	cagcagcagg	aggtaatctc	cgaaggcagc	600
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&lt;210&gt; 22

&lt;211&gt; 4321

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 22

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&lt;210&gt; 23

&lt;211&gt; 919

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 23

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Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser
 1      5      10      15
Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
 20      25      30
Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala Ala
 35      40      45
Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln Gln Gln Gln Gln Gln
 50      55      60
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Glu Thr
 65      70      75      80
Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly Glu Asp Gly Ser Pro Gln
 85      90      95
Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu Asp Glu Glu Gln
100      105      110
Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys His Pro Glu Arg Gly
115      120      125
Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala Ser Lys Gly Leu Pro
130      135      140
Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp Ser Ala Ala Pro Ser
145      150      155      160
Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser
165      170      175
Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser Thr Met Gln Leu Leu
180      185      190
Gln Gln Gln Gln Gln Glu Ala Val Ser Glu Gly Ser Ser Ser Gly Arg
195      200      205
Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser Lys Asp Asn Tyr Leu
210      215      220
Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys Glu Leu Cys Lys Ala
225      230      235      240
Val Ser Val Ser Met Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser
245      250      255
Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala Pro Leu Leu Gly
260      265      270
Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala Pro Leu Ala Glu Cys
275      280      285
Lys Gly Ser Leu Leu Asp Asp Ser Ala Gly Lys Ser Thr Glu Asp Thr
290      295      300
Ala Glu Tyr Ser Pro Phe Lys Gly Gly Tyr Thr Lys Gly Leu Glu Gly
305      310      315      320
Glu Ser Leu Gly Cys Ser Gly Ser Ala Ala Ala Gly Ser Ser Gly Thr
325      330      335
Leu Glu Leu Pro Ser Thr Leu Ser Leu Tyr Lys Ser Gly Ala Leu Asp
340      345      350
Glu Ala Ala Ala Tyr Gln Ser Arg Asp Tyr Tyr Asn Phe Pro Leu Ala
355      360      365
Leu Ala Gly Pro Pro Pro Pro Pro Pro Pro Pro His Pro His Ala Arg
370      375      380
Ile Lys Leu Glu Asn Pro Leu Asp Tyr Gly Ser Ala Trp Ala Ala Ala
385      390      395      400
Ala Ala Gln Cys Arg Tyr Gly Asp Leu Ala Ser Leu His Gly Ala Gly
405      410      415
Ala Ala Gly Pro Gly Ser Gly Ser Pro Ser Ala Ala Ala Ser Ser Ser
420      425      430
Trp His Thr Leu Phe Thr Ala Glu Glu Gly Gln Leu Tyr Gly Pro Cys
435      440      445
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
450      455      460

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Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Glu	Ala	Gly	Ala	Val	Ala	Pro	Tyr
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Gly	Tyr	Thr	Arg	Pro	Pro	Gln	Gly	Leu	Ala	Gly	Gln	Glu	Ser	Asp	Phe
				485					490					495	
Thr	Ala	Pro	Asp	Val	Trp	Tyr	Pro	Gly	Gly	Met	Val	Ser	Arg	Val	Pro
			500					505					510		
Tyr	Pro	Ser	Pro	Thr	Cys	Val	Lys	Ser	Glu	Met	Gly	Pro	Trp	Met	Asp
		515					520					525			
Ser	Tyr	Ser	Gly	Pro	Tyr	Gly	Asp	Met	Arg	Leu	Glu	Thr	Ala	Arg	Asp
		530				535					540				
His	Val	Leu	Pro	Ile	Asp	Tyr	Tyr	Phe	Pro	Pro	Gln	Lys	Thr	Cys	Leu
545					550				555						560
Ile	Cys	Gly	Asp	Glu	Ala	Ser	Gly	Cys	His	Tyr	Gly	Ala	Leu	Thr	Cys
			565						570						575
Gly	Ser	Cys	Lys	Val	Phe	Phe	Lys	Arg	Ala	Ala	Glu	Gly	Lys	Gln	Lys
			580					585					590		
Tyr	Leu	Cys	Ala	Ser	Arg	Asn	Asp	Cys	Thr	Ile	Asp	Lys	Phe	Arg	Arg
		595					600					605			
Lys	Asn	Cys	Pro	Ser	Cys	Arg	Leu	Arg	Lys	Cys	Tyr	Glu	Ala	Gly	Met
	610					615					620				
Thr	Leu	Gly	Ala	Arg	Lys	Leu	Lys	Lys	Leu	Gly	Asn	Leu	Lys	Leu	Gln
625					630					635					640
Glu	Glu	Gly	Glu	Ala	Ser	Ser	Thr	Thr	Ser	Pro	Thr	Glu	Glu	Thr	Thr
			645						650					655	
Gln	Lys	Leu	Thr	Val	Ser	His	Ile	Glu	Gly	Tyr	Glu	Cys	Gln	Pro	Ile
			660					665					670		
Phe	Leu	Asn	Val	Leu	Glu	Ala	Ile	Glu	Pro	Gly	Val	Val	Cys	Ala	Gly
		675					680					685			
His	Asp	Asn	Asn	Gln	Pro	Asp	Ser	Phe	Ala	Ala	Leu	Leu	Ser	Ser	Leu
	690					695					700				
Asn	Glu	Leu	Gly	Glu	Arg	Gln	Leu	Val	His	Val	Val	Lys	Trp	Ala	Lys
705					710					715					720
Ala	Leu	Pro	Gly	Phe	Arg	Asn	Leu	His	Val	Asp	Asp	Gln	Met	Ala	Val
			725						730					735	
Ile	Gln	Tyr	Ser	Trp	Met	Gly	Leu	Met	Val	Phe	Ala	Met	Gly	Trp	Arg
			740					745					750		
Ser	Phe	Thr	Asn	Val	Asn	Ser	Arg	Met	Leu	Tyr	Phe	Ala	Pro	Asp	Leu
		755					760					765			
Val	Phe	Asn	Glu	Tyr	Arg	Met	His	Lys	Ser	Arg	Met	Tyr	Ser	Gln	Cys
	770					775					780				
Val	Arg	Met	Arg	His	Leu	Ser	Gln	Glu	Phe	Gly	Trp	Leu	Gln	Ile	Thr
785					790					795					800
Pro	Gln	Glu	Phe	Leu	Cys	Met	Lys	Ala	Leu	Leu	Leu	Phe	Ser	Ile	Ile
			805						810					815	
Pro	Val	Asp	Gly	Leu	Lys	Asn	Gln	Lys	Phe	Phe	Asp	Glu	Leu	Arg	Met
			820					825					830		
Asn	Tyr	Ile	Lys	Glu	Leu	Asp	Arg	Ile	Ile	Ala	Cys	Lys	Arg	Lys	Asn
		835					840					845			
Pro	Thr	Ser	Cys	Ser	Arg	Arg	Phe	Tyr	Gln	Leu	Thr	Lys	Leu	Leu	Asp
	850					855					860				
Ser	Val	Gln	Pro	Ile	Ala	Arg	Glu	Leu	His	Gln	Phe	Thr	Phe	Asp	Leu
865					870					875					880
Leu	Ile	Lys	Ser	His	Met	Val	Ser	Val	Asp	Phe	Pro	Glu	Met	Met	Ala
			885						890					895	
Glu	Ile	Ile	Ser	Val	Gln	Val	Pro	Lys	Ile	Leu	Ser	Gly	Lys	Val	Lys
			900					905					910		
Pro	Ile	Tyr	Phe	His	Thr	Gln									
		915													

&lt;210&gt; 24

&lt;211&gt; 595

<213> Artificial Sequence

<223> Description of Artificial Sequence:/note =  
synthetic construct

Met 1	Thr	Met	Thr	Leu 5	His	Thr	Lys	Ala	Ser 10	Gly	Met	Ala	Leu	Leu 15	His
Gln	Ile	Gln	Gly 20	Asn	Glu	Leu	Glu	Pro 25	Leu	Asn	Arg	Pro	Gln 30	Leu	Lys
Ile	Pro	Leu 35	Glu	Arg	Pro	Leu	Gly 40	Glu	Val	Tyr	Leu 45	Asp	Ser	Ser	Lys
Pro	Ala 50	Val	Tyr	Asn	Tyr	Pro 55	Glu	Gly	Ala	Ala	Tyr 60	Glu	Phe	Asn	Ala
Ala 65	Ala	Ala	Ala	Asn 70	Ala	Gln	Val	Tyr	Gly	Gln 75	Thr	Gly	Leu	Pro	Tyr 80
Gly	Pro	Gly	Ser 85	Glu	Ala	Ala	Ala	Phe 90	Gly	Ser	Asn	Gly	Leu	Gly 95	Gly
Phe	Pro	Pro	Leu 100	Asn	Ser	Val	Ser	Pro 105	Ser	Pro	Leu	Met	Leu 110	Leu	His
Pro	Pro	Pro 115	Gln	Leu	Ser	Pro	Phe 120	Leu	Gln	Pro	His 125	Gly	Gln	Gln	Val
Pro	Tyr 130	Tyr	Leu	Glu	Asn 135	Glu	Pro	Ser	Gly	Tyr	Thr 140	Val	Arg	Glu	Ala
Gly 145	Pro	Pro	Ala	Phe 150	Tyr	Arg	Pro	Asn	Ser	Asp 155	Asn	Arg	Arg	Gln	Gly 160
Gly	Arg	Glu	Arg 165	Leu	Ala	Ser	Thr	Asn 170	Asp	Lys	Gly	Ser	Met	Ala 175	Met
Glu	Ser	Ala	Lys 180	Glu	Thr	Arg	Tyr	Cys 185	Ala	Val	Cys	Asn	Asp 190	Tyr	Ala
Ser	Gly	Tyr 195	His	Tyr	Gly	Val	Trp 200	Ser	Cys	Glu	Gly 205	Cys	Lys	Ala	Phe
Phe	Lys 210	Arg	Ser	Ile	Gln	Gly 215	His	Asn	Asp	Tyr	Met 220	Cys	Pro	Ala	Thr
Asn 225	Gln	Cys	Thr	Ile 230	Asp	Lys	Asn	Arg	Arg	Lys 235	Ser	Cys	Gln	Ala	Cys 240
Arg	Leu	Arg	Lys 245	Cys	Tyr	Glu	Val	Gly	Met 250	Met	Lys	Gly	Gly	Ile 255	Arg
Lys	Asp	Arg	Arg 260	Gly	Gly	Arg	Met	Leu 265	Lys	His	Lys	Arg	Gln 270	Arg	Asp
Asp	Gly	Glu 275	Gly	Arg	Gly	Glu	Val 280	Gly	Ser	Ala	Gly 285	Asp	Met	Arg	Ala
Ala	Asn 290	Leu	Trp	Pro	Ser	Pro 295	Leu	Met	Ile	Lys	Arg 300	Ser	Lys	Lys	Asn
Ser 305	Leu	Ala	Leu	Ser 310	Leu	Thr	Ala	Asp	Gln	Met 315	Val	Ser	Ala	Leu	Leu 320
Asp	Ala	Glu	Pro 325	Pro	Ile	Leu	Tyr	Ser	Glu 330	Tyr	Asp	Pro	Thr	Arg 335	Pro
Phe	Ser	Glu	Ala 340	Ser	Met	Met	Gly	Leu 345	Leu	Thr	Asn	Leu	Ala 350	Asp	Arg
Glu	Leu	Val 355	His	Met	Ile	Asn	Trp 360	Ala	Lys	Arg	Val	Pro 365	Gly	Phe	Val
Asp 370	Leu	Thr	Leu	His 375	Asp	Gln	Val	His	Leu	Leu	Glu 380	Cys	Ala	Trp	Leu
Glu 385	Ile	Leu	Met	Ile 390	Gly	Leu	Val	Trp	Arg	Ser 395	Met	Glu	His	Pro	Val 400
Lys	Leu	Leu	Phe 405	Ala	Pro	Asn	Leu	Leu 410	Leu	Asp	Arg	Asn	Gln 415	Gly	Lys

Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser  
 420 425 430  
 Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu  
 435 440 445  
 Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser  
 450 455 460  
 Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp  
 465 470 475 480  
 Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr  
 485 490 495  
 Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser  
 500 505 510  
 His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met  
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 Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu  
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 Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val  
 545 550 555 560  
 Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser  
 565 570 575  
 His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro  
 580 585 590  
 Ala Thr Val  
 595

&lt;210&gt; 25

&lt;211&gt; 6450

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
 synthetic construct

&lt;400&gt; 25

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agtggattca	ggaatctggg	gaatggcaaa	tatattaaga	agagtattga	aagtatttgg	4980
aggaaaatgg	tttaattctg	gtgtgcacca	aggttcagta	gagtcacttt	ctgccctgga	5040
gaccacaaat	caactagctc	catttacagc	catttctaaa	atggcagctt	cagttctaga	5100
gaagaaagaa	caacatcagc	agtaaagtcc	atggaatagc	tagtggtctg	tgtttctttt	5160
cgccattgcc	tagcttgccg	taatgattct	ataatgccat	catgcagcaa	ttatgagagg	5220

```

ctagggtcatc caaagagaag accctatcaa tgtagggttcg aaaatctaac ccctaaggaa 5280
gtgcagtcctt tgatttgatt tccctagtaa ccttgcatg atgtttaacc aagccatagc 5340
ccatgccttt tgagggctga acaaataagg gacttactga taatttactt ttgatcacat 5400
taagggtgttc tcaccttgaa atcttataca ctgaaatggc cattgattta ggccactggc 5460
ttagagtact ccttccctg catgacactg attacaaata ctttcctatt catactttcc 5520
aattatgaga tggactgtgg gtactgggag tgatcactaa caccatagta atgtctaata 5580
ttcacaggca gatctgcttg gggagctag ttatgtgaaa ggcaaataaa gtcatacagt 5640
agctcaaaaag gcaaccataa ttctctttgg tgcaagtctt gggagcgtga tctagattac 5700
actgcaccat tcccaagtta atcccctgaa aacttactct caactggagc aaatgaactt 5760
tgggtcccaaa tatccatctt ttcagtagcg ttaattatgc tctgtttcca actgcatttc 5820
ctttccaatt gaattaaagt gtggcctcgt ttttagtcat ttaaaattgt tttctaagta 5880
attgctgcct ctattatggc acttcaattt tgcactgtct tttgagattc aagaaaaatt 5940
tctattcatt tttttgcac caattgtgcc tgaactttta aaatatgtaa atgctgccat 6000
gttccaaacc catcgtcagt gtgtgtgttt agagctgtgc accctagaaa caacatactt 6060
gtcccatgag caggtgcctg agacacagac ccctttgcat tcacagagag gtcattgggt 6120
atagagactt gaattaataa gtgacattat gccagtttct gttctctcac aggtgataaa 6180
caatgctttt tgtgcactac atactcttca gtgtagagct cttgttttat gggaaaaggc 6240
tcaaatgcca aattgtgttt gatggattaa tatgcccttt tgccgatgca tactattact 6300
gatgtgactc ggttttgcg cagctttgct ttgtttaatg aaacacactt gtaaacctct 6360
tttgactttt gaaaaagaat ccagcgggat gctcgagcac ctgtaaaaaa ttttctcaac 6420
ctatttgatg ttcaataaaa gaattaaact 6450

```

<210> 26

<211> 614

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 26

```

Met Asn Thr Phe Gln Asp Gln Ser Gly Ser Ser Ser Asn Arg Glu Pro
1          5          10          15
Leu Leu Arg Cys Ser Asp Ala Arg Arg Asp Leu Glu Leu Ala Ile Gly
20          25          30
Gly Val Leu Arg Ala Glu Gln Gln Ile Lys Asp Asn Leu Arg Glu Val
35          40          45
Lys Ala Gln Ile His Ser Cys Ile Ser Arg His Leu Glu Cys Leu Arg
50          55          60
Ser Arg Glu Val Trp Leu Tyr Glu Gln Val Asp Leu Ile Tyr Gln Leu
65          70          75          80
Lys Glu Glu Thr Leu Gln Gln Gln Ala Gln Gln Leu Tyr Ser Leu Leu
85          90          95
Gly Gln Phe Asn Cys Leu Thr His Gln Leu Glu Cys Thr Gln Asn Lys
100         105         110
Asp Leu Ala Asn Gln Val Ser Val Cys Leu Glu Arg Leu Gly Ser Leu
115         120         125
Thr Leu Lys Pro Glu Asp Ser Thr Val Leu Leu Phe Glu Ala Asp Thr
130         135         140
Ile Thr Leu Arg Gln Thr Ile Thr Thr Phe Gly Ser Leu Lys Thr Ile
145         150         155         160
Gln Ile Pro Glu His Leu Met Ala His Ala Ser Ser Ala Asn Ile Gly
165         170         175
Pro Phe Leu Glu Lys Arg Gly Cys Ile Ser Met Pro Glu Gln Lys Ser
180         185         190
Ala Ser Gly Ile Val Ala Val Pro Phe Ser Glu Trp Leu Leu Gly Ser
195         200         205

```

Lys Pro Ala Ser Gly Tyr Gln Ala Pro Tyr Ile Pro Ser Thr Asp Pro  
 210 215 220  
 Gln Asp Trp Leu Thr Gln Lys Gln Thr Leu Glu Asn Ser Gln Thr Ser  
 225 230 235 240  
 Ser Arg Ala Cys Asn Phe Phe Asn Asn Val Gly Gly Asn Leu Lys Gly  
 245 250 255  
 Leu Glu Asn Trp Leu Leu Lys Ser Glu Lys Ser Ser Tyr Gln Lys Cys  
 260 265 270  
 Asn Ser His Ser Thr Thr Ser Ser Phe Ser Ile Glu Met Glu Lys Val  
 275 280 285  
 Gly Asp Gln Glu Leu Pro Asp Gln Asp Glu Met Asp Leu Ser Asp Trp  
 290 295 300  
 Leu Val Thr Pro Gln Glu Ser His Lys Leu Arg Lys Pro Glu Asn Gly  
 305 310 315 320  
 Ser Arg Glu Thr Ser Glu Lys Phe Lys Leu Leu Phe Gln Ser Tyr Asn  
 325 330 335  
 Val Asn Asp Trp Leu Val Lys Thr Asp Ser Cys Thr Asn Cys Gln Gly  
 340 345 350  
 Asn Gln Pro Lys Gly Val Glu Ile Glu Asn Leu Gly Asn Leu Lys Cys  
 355 360 365  
 Leu Asn Asp His Leu Glu Ala Lys Lys Pro Leu Ser Thr Pro Ser Met  
 370 375 380  
 Val Thr Glu Asp Trp Leu Val Gln Asn His Gln Asp Pro Cys Lys Val  
 385 390 395 400  
 Glu Glu Val Cys Arg Ala Asn Glu Pro Cys Thr Ser Phe Ala Glu Cys  
 405 410 415  
 Val Cys Asp Glu Asn Cys Glu Lys Glu Ala Leu Tyr Lys Trp Leu Leu  
 420 425 430  
 Lys Lys Glu Gly Lys Asp Lys Asn Gly Met Pro Val Glu Pro Lys Pro  
 435 440 445  
 Glu Pro Glu Lys His Lys Asp Ser Leu Asn Met Trp Leu Cys Pro Arg  
 450 455 460  
 Lys Glu Val Ile Glu Gln Thr Lys Ala Pro Lys Ala Met Thr Pro Ser  
 465 470 475 480  
 Arg Ile Ala Asp Ser Phe Gln Val Ile Lys Asn Ser Pro Leu Ser Glu  
 485 490 495  
 Trp Leu Ile Arg Pro Pro Tyr Lys Glu Gly Ser Pro Lys Glu Val Pro  
 500 505 510  
 Gly Thr Glu Asp Arg Ala Gly Lys Gln Lys Phe Lys Ser Pro Met Asn  
 515 520 525  
 Thr Ser Trp Cys Ser Phe Asn Thr Ala Asp Trp Val Leu Pro Gly Lys  
 530 535 540  
 Lys Met Gly Asn Leu Ser Gln Leu Ser Ser Gly Glu Asp Lys Trp Leu  
 545 550 555 560  
 Leu Arg Lys Lys Ala Gln Glu Val Leu Leu Asn Ser Pro Leu Gln Glu  
 565 570 575  
 Glu His Asn Phe Pro Pro Asp His Tyr Gly Leu Pro Ala Val Cys Asp  
 580 585 590  
 Leu Phe Ala Cys Met Gln Leu Lys Val Asp Lys Glu Lys Trp Leu Tyr  
 595 600 605  
 Arg Thr Pro Leu Gln Met  
 610

&lt;210&gt; 27

&lt;211&gt; 1845

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence:/note =  
 synthetic construct



&lt;400&gt; 27

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atgaatacct tccaagacca gaggggcagc tccagtaata gagaaccctt tttgaggtgt      60
agtgatgcac ggagggactt ggagcttgct attggtggag ttctccgggc tgaacagcaa      120
attaaagata acttgcgaga ggtcaaagct cagattcaca gttgcataag ccgtcacctg      180
gaatgtctta gaagccgtga ggtatggctg tatgaacagg tggaccttat ttatcagctt      240
aaagaggaga cacttcaaca gcaggctcag cagctctact cgttattggg ccagttcaat      300
tgtcttactc atcaactgga gtgtacccaa aacaaagatc tagccaatca agtctctgtg      360
tgcctggaga gactgggcag tttgaccctt aagcctgaag attcaactgt cctgctcttt      420
gaagctgaca caattactct gcgccagacc atcaccacat ttgggtctct caaaaccatt      480
caaattcctg agcacttgat ggctcatgct agttcagcaa atattgggcc cttcctggag      540
aagagaggct gtatctccat gccagagcag aagtcagcat ccggtattgt agctgtccct      600
ttcagcgaat ggctccttgg aagcaaacct gccagtgggt atcaagctcc ttacataccc      660
agcaccgacc cccaggactg gcttacccaa aagcagacct tggagaacag tcagacttct      720
tccagagcct gcaatttctt caataatgtc gggggaaacc taaagggtt agaaaactgg      780
ctcctcaaga gtgaaaaatc aagttatcaa aagtgtaaac gccattccac tactagtctt      840
ttctccattg aaatggaaaa ggttggagat caagagcttc ctgatcaaga tgagatggac      900
ctatcagatt ggctagtgaac tccccaggaa tcccataagc tgcggaagcc tgagaatggc      960
agtcgtgaaa ccagtggagaa gtttaagctc ttattccagt cctataatgt gaatgattgg      1020
cttgtcaaga ctgactctg taccaactgt cagggaacc agcccaaagg tgtggagatt      1080
gaaaacctgg gcaatctgaa gtgcctgaat gaccacttgg aggccaaaga accattgtcc      1140
acccccagca tggttacaga ggattggctt gtccagaacc atcaggaccc atgtaaggta      1200
gaggaggtgt gcagagccaa tgagccctgc acaagcttgg cagagtgtgt gtgtgatgag      1260
aattgtgaga aggaggtctt gtataagtgg cttctgaaga aagaaggaaa ggataaaaat      1320
gggatgcctg tggaacccaa acctgagcct gagaagcata aagattccct gaatatgtgg      1380
ctctgtccta gaaaagaagt aatagaacaa actaaagcac caaaggcaat gactccttct      1440
agaattgctg attccttcca agtcataaag aacagccctt tgtcggagtg gcttatcagg      1500
ccccataca aagaagggaag tcccaaggaa gtgcctggta ctgaagacag agctggcaaa      1560
cagaagttta aaagcccat gaatacttcc tgggtgttcc ttaacacagc tgactgggtc      1620
ctgccaggaa agaagatggg caacctcagc cagttatctt ctggagaaga caagtggctg      1680
cttcgaaaga aggccagga agtattactt aattcacctc tacaggagga acataacttc      1740
ccccagacc attatggcct ccctgcagtt tgtgatctct ttgcctgtat gcagcttaaa      1800
gttgataaag agaagtgggt atatcgaact cctctacaga tgtga                          1845

```

&lt;210&gt; 28

&lt;211&gt; 474

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 28

```

Met Ser Ser Glu Asp Arg Glu Ala Gln Glu Asp Glu Leu Leu Ala Leu
 1              5              10              15
Ala Ser Ile Tyr Asp Gly Asp Glu Phe Arg Lys Ala Glu Ser Val Gln
 20              25              30
Gly Gly Glu Thr Arg Ile Tyr Leu Asp Leu Pro Gln Asn Phe Lys Ile
 35              40              45
Phe Val Ser Gly Asn Ser Asn Glu Cys Leu Gln Asn Ser Gly Phe Glu
 50              55              60
Tyr Thr Ile Cys Phe Leu Pro Pro Leu Val Leu Asn Phe Glu Leu Pro
 65              70              75              80
Pro Asp Tyr Pro Ser Ser Ser Pro Pro Ser Phe Thr Leu Ser Gly Lys
 85              90              95
Trp Leu Ser Pro Thr Gln Leu Ser Ala Leu Cys Lys His Leu Asp Asn
100              105              110
Leu Trp Glu His Arg Gly Ser Val Val Leu Phe Ala Trp Met Gln
115              120              125

```

Phe Leu Lys Glu Glu Thr Leu Ala Tyr Leu Asn Ile Val Ser Pro Phe  
 130 135 140  
 Glu Leu Lys Ile Gly Ser Gln Lys Lys Val Gln Arg Arg Thr Ala Gln  
 145 150 155 160  
 Ala Ser Pro Asn Thr Glu Leu Asp Phe Gly Gly Ala Ala Gly Ser Asp  
 165 170 175  
 Val Asp Gln Glu Glu Ile Val Asp Glu Arg Ala Val Gln Asp Val Glu  
 180 185 190  
 Ser Leu Ser Asn Leu Ile Gln Glu Ile Leu Asp Phe Asp Gln Ala Gln  
 195 200 205  
 Gln Ile Lys Cys Phe Asn Ser Lys Leu Phe Leu Cys Ser Ile Cys Phe  
 210 215 220  
 Cys Glu Lys Leu Gly Ser Glu Cys Met Tyr Phe Leu Glu Cys Arg His  
 225 230 235 240  
 Val Tyr Cys Lys Ala Cys Leu Lys Asp Tyr Phe Glu Ile Gln Ile Arg  
 245 250 255  
 Asp Gly Gln Val Gln Cys Leu Asn Cys Pro Glu Pro Lys Cys Pro Ser  
 260 265 270  
 Val Ala Thr Pro Gly Gln Val Lys Glu Leu Val Glu Ala Glu Leu Phe  
 275 280 285  
 Ala Arg Tyr Asp Arg Leu Leu Leu Gln Ser Ser Leu Asp Leu Met Ala  
 290 295 300  
 Asp Val Val Tyr Cys Pro Arg Pro Cys Cys Gln Leu Pro Val Met Gln  
 305 310 315 320  
 Glu Pro Gly Cys Thr Met Gly Ile Cys Ser Ser Cys Asn Phe Ala Phe  
 325 330 335  
 Cys Thr Leu Cys Arg Leu Thr Tyr His Gly Val Ser Pro Cys Lys Val  
 340 345 350  
 Thr Ala Glu Lys Leu Met Asp Leu Arg Asn Glu Tyr Leu Gln Ala Asp  
 355 360 365  
 Glu Ala Asn Lys Arg Leu Leu Asp Gln Arg Tyr Gly Lys Arg Val Ile  
 370 375 380  
 Gln Lys Ala Leu Glu Glu Met Glu Ser Lys Glu Trp Leu Glu Lys Asn  
 385 390 395 400  
 Ser Lys Ser Cys Pro Cys Cys Gly Thr Pro Ile Glu Lys Leu Asp Gly  
 405 410 415  
 Cys Asn Lys Met Thr Cys Thr Gly Cys Met Gln Tyr Phe Cys Trp Ile  
 420 425 430  
 Cys Met Gly Ser Leu Ser Arg Ala Asn Pro Tyr Lys His Phe Asn Asp  
 435 440 445  
 Pro Gly Ser Pro Cys Phe Asn Arg Leu Phe Tyr Ala Val Asp Val Asp  
 450 455 460  
 Asp Asp Ile Trp Glu Asp Glu Val Glu Asp  
 465 470

<210> 29

<211> 1701

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 29

ggctctctggt	ctcccctctc	tgagcactct	gaggtcctta	tgctcgtcaga	agatcgagaa	60
gctcaggagg	atgaattgct	ggccctggca	agtatttacg	atggagatga	atttagaaaa	120
gcagagtctg	tccaaggtgg	agaaaccagg	atctatttgg	atttgccaca	gaatttcaag	180
atatttgtga	gcggcaattc	aaatgagtgt	ctccagaata	gtggctttga	atacaccatt	240
tgctttctgc	ctccacttgt	gctgaacttt	gaactgccac	cagattatcc	atcctcttcc	300
ccaccttcat	tcacacttag	tggcaaatgg	ctgtcaccaa	ctcagctatc	tgctctatgc	360

```

aagcacttag acaacctatg ggaagaacac cgtggcagcg tggtcctggt tgcctggatg      420
caattttctta aggaagagac cctagcatatc ttgaatatgt tctctccttt tgagctcaag      480
attggttctc agaaaaaagt gcagagaagg acagctcaag cttctcccaa cacagagcta      540
gattttggag gagctgctgg atctgatgta gaccaagagg aaattgtgga tgagagagca      600
gtgcaggatg tggaaatcact gtcaaactctg atccaggaaa tcttggactt tgatcaagct      660
cagcagataa aatgctttta tagtaaattg ttcctgtgca gtatctgttt ctgtgagaag      720
ctgggtagtg aatgcatgta cttcttggag tgcaggcatg tgtactgcaa agcctgtctg      780
aaggactact ttgaaatcca gatcagagat ggccagggttc aatgcctcaa ctgcccagaa      840
ccaaagtgcc cttcgggtggc cactcctggt cctcctccag tcctccttgg acctgatggc agatgtggtg      900
tttgcccgtt atgaccgcct tctcctccag gtgatgcagg aacctggctg caccatgggt      960
tactgcccc ggccgtgctg ccagctgcct gtgatgcagg aacctggctg caccatgggt      1020
atctgctcca gctgcaatgt tgccttctgt actttgtgca ggttgacctt ccatggggtc      1080
tccccatgta aggtgactgc agagaaatta atggacttac gaaatgaata cctgcaagcg      1140
gatgaggcta ataaaagact tttggatcaa aggtatggta agagagtgat tcagaaggca      1200
ctggaagaga tggaaagtaa ggagtggcta gagaagaact caaagagctg cccatgttgt      1260
ggaactccca tagagaaatt agacggatgt aacaagatga catgtactgg ctgtatgcaa      1320
tattttctgtt ggatttgcac gggttctctc tctagagcaa acccttacia acatttcaat      1380
gaccctgggt caccatgttt taaccggctg ttttatgctg tggatgttga cgacgatatt      1440
tggaagatg aggtagaaga ctagttaact actgctcaag atatggaagt ggattgtttt      1500
tccctaattc tccgtcaagt acacaaagta actttgcggg atatttaggg tactattcat      1560
tcaactcttc tgcgtagaag atatggaaga acgaggttta tattttcatg tgggtactact      1620
gaagaagggt cattgatata tttttaaatg taagttgaga aaaatttata agccaaagg      1680
tcagaaaatt aaactacaga a                                     1701

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&lt;210&gt; 30

&lt;211&gt; 444

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 30

```

Met Pro Arg Ser Gly Ala Pro Lys Glu Arg Pro Ala Glu Pro Leu Thr
1          5          10          15
Pro Pro Pro Ser Tyr Gly His Gln Pro Gln Thr Gly Ser Gly Glu Ser
20          25          30
Ser Gly Ala Ser Gly Asp Lys Asp His Leu Tyr Ser Thr Val Cys Lys
35          40          45
Pro Arg Ser Pro Lys Pro Ala Ala Pro Ala Ala Pro Pro Phe Ser Ser
50          55          60
Ser Ser Gly Val Leu Gly Thr Gly Leu Cys Glu Leu Asp Arg Leu Leu
65          70          75          80
Gln Glu Leu Asn Ala Thr Gln Phe Asn Ile Thr Asp Glu Ile Met Ser
85          90          95
Gln Phe Pro Ser Ser Lys Val Ala Ser Gly Glu Gln Lys Glu Asp Gln
100         105         110
Ser Glu Asp Lys Lys Arg Pro Ser Leu Pro Ser Ser Pro Ser Pro Gly
115         120         125
Leu Pro Lys Ala Ser Ala Thr Ser Ala Thr Leu Glu Leu Asp Arg Leu
130         135         140
Met Ala Ser Leu Pro Asp Phe Arg Val Gln Asn His Leu Pro Ala Ser
145         150         155         160
Gly Pro Thr Gln Pro Pro Val Val Ser Ser Thr Asn Glu Gly Ser Pro
165         170         175
Ser Pro Pro Glu Pro Thr Ala Lys Gly Ser Leu Asp Thr Met Leu Gly
180         185         190
Leu Leu Gln Ser Asp Leu Ser Arg Arg Gly Val Pro Thr Gln Ala Lys
195         200         205

```

Gly Leu Cys Gly Ser Cys Asn Lys Pro Ile Ala Gly Gln Val Val Thr  
 210 215 220  
 Ala Leu Gly Arg Ala Trp His Pro Glu His Phe Val Cys Gly Gly Cys  
 225 230 235 240  
 Ser Thr Ala Leu Gly Gly Ser Ser Phe Phe Glu Lys Asp Gly Ala Pro  
 245 250 255  
 Phe Cys Pro Glu Cys Tyr Phe Glu Arg Phe Ser Pro Arg Cys Gly Phe  
 260 265 270  
 Cys Asn Gln Pro Ile Arg His Lys Met Val Thr Ala Leu Gly Thr His  
 275 280 285  
 Trp His Pro Glu His Phe Cys Cys Val Ser Cys Gly Glu Pro Phe Gly  
 290 295 300  
 Asp Glu Gly Phe His Glu Arg Glu Gly Arg Pro Tyr Cys Arg Arg Asp  
 305 310 315 320  
 Phe Leu Gln Leu Phe Ala Pro Arg Cys Gln Gly Cys Gln Gly Pro Ile  
 325 330 335  
 Leu Asp Asn Tyr Ile Ser Ala Leu Ser Leu Leu Trp His Pro Asp Cys  
 340 345 350  
 Phe Val Cys Arg Glu Cys Phe Ala Pro Phe Ser Gly Gly Ser Phe Phe  
 355 360 365  
 Glu His Glu Gly Arg Pro Leu Cys Glu Asn His Phe His Ala Arg Arg  
 370 375 380  
 Gly Ser Leu Trp Pro Thr Cys Gly Leu Pro Val Thr Gly Arg Cys Val  
 385 390 395 400  
 Ser Ala Leu Gly Arg Arg Phe His Pro Asp His Phe Ala Cys Thr Phe  
 405 410 415  
 Cys Leu Arg Pro Leu Thr Lys Gly Ser Phe Gln Glu Arg Ala Gly Lys  
 420 425 430  
 Pro Tyr Cys Gln Pro Cys Phe Leu Lys Leu Phe Gly  
 435 440

<210> 31

<211> 1335

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 31

atgccaaagg	caggggctcc	caaagagcgc	cctgcgggagc	ctctcacc	ccccatcc	60
tatggccacc	agccacagac	agggctctggg	gagtcctcag	gagcctcggg	ggacaaggac	120
cacctgtaca	gcacggtatg	caagcctcgg	tccccaaagc	ctgcagcccc	ggcgcgccct	180
ccattctcct	cttcagcgg	tgtcttgggt	accgggctct	gtgagctaga	tcggttgctt	240
caggaactta	atgccactca	gttcaacatc	acagatgaaa	tcatgtctca	gttcccatct	300
agcaagggtg	cttcaggaga	gcagaaggag	gaccagtctg	aagataagaa	aagacccagc	360
ctcccttcca	gcccgtctcc	tggcctccca	aaggcttctg	ccacctcagc	cactctggag	420
ctggatagac	tgatggcctc	actccctgac	tccgcggttc	aaaaccatct	tccagcctct	480
gggccaactc	agccaccggt	ggtgagctcc	acaaatgagg	gctccccatc	cccaccagag	540
ccgactgcaa	agggcagcct	agacaccatg	ctggggctgc	tgcagtcgga	cctcagccgc	600
cgggggtgtc	ccaccacggc	caaaggcctc	tgtggctcct	gcaataaacc	tattgctggg	660
caagtgggtga	cggctctggg	ccgcgcctgg	caccccgagc	acttcgtttg	cggaggctgt	720
tccaccgccc	tgggaggcag	cagcttcttc	gagaaggatg	gagccccctt	ctgccccgag	780
tgctactttg	agcgcttctc	gccaagatgt	ggcttctgca	accagcccat	ccgacacaag	840
atgggtgaccg	ccttgggcac	tactggcac	ccagagcatt	tctgctgcgt	cagttgcggg	900
gagcccttcg	gagatgaggg	tttccacgag	cgcgagggcc	gcccctactg	ccgccgggac	960
ttcctgcagc	tgttcgcccc	gcgctgccag	ggctgccagg	gccccatcct	ggataactac	1020
atctcggcgc	tcagcctgct	ctggcaccgc	gactgtttcg	tctgcaggga	atgcttcgcg	1080
cccttctcgg	gaggcagctt	tttcgagcac	gagggcgcgc	cgttgtgcga	gaaccacttc	1140
cacgcacgac	gcggctcgct	gtggcccacg	tgtggcctcc	ctgtgaccgc	ccgctgcgtg	1200

```

tcggccctgg gtcgccgctt ccacccggac cacttcgcat gcaccttctg cctgcgcccg 1260
ctcaccaagg ggtccttcca ggagcgcgcc ggcaagccct actgccagcc ctgcttcctg 1320
aagctcttcg gctga 1335

```

&lt;210&gt; 32

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 32

```

Met Ala Ala Gln Gly Glu Pro Gln Val Gln Phe Lys Leu Val Leu Val
1      5      10      15
Gly Asp Gly Gly Thr Gly Lys Thr Thr Phe Val Lys Arg His Leu Thr
20     25     30
Gly Glu Phe Glu Lys Lys Tyr Val Ala Thr Leu Gly Val Glu Val His
35     40     45
Pro Leu Val Phe His Thr Asn Arg Gly Pro Ile Lys Phe Asn Val Trp
50     55     60
Asp Thr Ala Gly Gln Glu Lys Phe Gly Gly Leu Arg Asp Gly Tyr Tyr
65     70     75     80
Ile Gln Ala Gln Cys Ala Ile Ile Met Phe Asp Val Thr Ser Arg Val
85     90     95
Thr Tyr Lys Asn Val Pro Asn Trp His Arg Asp Leu Val Arg Val Cys
100    105    110
Glu Asn Ile Pro Ile Val Leu Cys Gly Asn Lys Val Asp Ile Lys Asp
115    120    125
Arg Lys Val Lys Ala Lys Ser Ile Val Phe His Arg Lys Lys Asn Leu
130    135    140
Gln Tyr Tyr Asp Ile Ser Ala Lys Ser Asn Tyr Asn Phe Glu Lys Pro
145    150    155    160
Phe Leu Trp Leu Ala Arg Lys Leu Ile Gly Asp Pro Asn Leu Glu Phe
165    170    175
Val Ala Met Pro Ala Leu Ala Pro Pro Glu Val Val Met Asp Pro Ala
180    185    190
Leu Ala Ala Gln Tyr Glu His Asp Leu Glu Val Ala Gln Thr Thr Ala
195    200    205
Leu Pro Asp Glu Asp Asp Asp Leu
210    215

```

&lt;210&gt; 33

&lt;211&gt; 1566

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 33

```

ggcgcttctg gaaggaacgc cgcgatggct gcgcagggag agccccaggt ccagttcaaa 60
cttgatttgg ttggtgatgg tggtagcacc aaaacgacct tcgtgaaacg tcatttgact 120
ggtgaatttg agaagaagta tgtagccacc ttgggtggtg aggttcatcc cctagtgttc 180
cacaccaaca gaggacctat taagttcaat gtatgggaca cagccggcca ggagaaattc 240
ggtggactga gagatggcta ttatatccaa gcccagtggt ccatcataat gtttgatgta 300
acatcgagag ttacttacaa gaatgtgcct aactggcata gagatctggt acgagtgtgt 360
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<211> 2427

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
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<400> 34

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Ser Thr Ser Gln Glu Leu Pro Phe Cys Gln Pro Lys Lys Lys Ser Thr
 35          40          45
Pro Leu Lys Tyr Glu Val Gly Asp Leu Ile Trp Ala Lys Phe Lys Arg
 50          55          60
Arg Pro Trp Trp Pro Cys Arg Ile Cys Ser Asp Pro Leu Ile Asn Thr
 65          70          75          80
His Ser Lys Met Lys Val Ser Asn Arg Arg Pro Tyr Arg Gln Tyr Tyr
 85          90          95
Val Glu Ala Phe Gly Asp Pro Ser Glu Arg Ala Trp Val Ala Gly Lys
100          105          110
Ala Ile Val Met Phe Glu Gly Arg His Gln Phe Glu Glu Leu Pro Val
115          120          125
Leu Arg Arg Arg Gly Lys Gln Lys Glu Lys Gly Tyr Arg His Lys Val
130          135          140
Pro Gln Lys Ile Leu Ser Lys Trp Glu Ala Ser Val Gly Leu Ala Glu
145          150          155          160
Gln Tyr Asp Val Pro Lys Gly Ser Lys Asn Arg Lys Cys Ile Pro Gly
165          170          175
Ser Ile Lys Leu Asp Ser Glu Glu Asp Met Pro Phe Glu Asp Cys Thr
180          185          190
Asn Asp Pro Glu Ser Glu His Asp Leu Leu Leu Asn Gly Cys Leu Lys
195          200          205
Ser Leu Ala Phe Asp Ser Glu His Ser Ala Asp Glu Lys Glu Lys Pro
210          215          220
Cys Ala Lys Ser Arg Ala Arg Lys Ser Ser Asp Asn Pro Lys Arg Thr
225          230          235          240

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Ile	Ser	Asp	Thr	Gln	Ala	Ser	Asn	Glu	Leu	Ser	Arg	Ile	Ala	Asn	Ser	275	280	285
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Gly	Lys	Asn	Thr	Ala	Lys	Lys	Glu	Phe	Glu	Thr	Ser	Asn	Gly	Asp	Ser	305	310	315
Leu	Leu	Gly	Leu	Pro	Glu	Gly	Ala	Leu	Ile	Ser	Lys	Cys	Ser	Arg	Glu	325	330	335
Lys	Asn	Lys	Pro	Gln	Arg	Ser	Leu	Val	Cys	Gly	Ser	Lys	Val	Lys	Leu	340	345	350
Cys	Tyr	Ile	Gly	Ala	Gly	Asp	Glu	Glu	Lys	Arg	Ser	Asp	Ser	Ile	Ser	355	360	365
Ile	Cys	Thr	Thr	Ser	Asp	Asp	Gly	Ser	Ser	Asp	Leu	Asp	Pro	Ile	Glu	370	375	380
His	Ser	Ser	Glu	Ser	Asp	Asn	Ser	Val	Leu	Glu	Ile	Pro	Asp	Ala	Phe	385	390	395
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Tyr	Ser	Arg	Phe	Ala	Ala	Thr	Asn	Thr	Arg	Val	Lys	Ala	Lys	Gln	Lys	420	425	430
Pro	Leu	Ile	Ser	Asn	Ser	His	Thr	Asp	His	Leu	Met	Gly	Cys	Thr	Lys	435	440	445
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&lt;210&gt; 36

&lt;211&gt; 2696

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 36

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Ser	Asn	Pro	Val	Asn	Leu	Asp	Ala	Pro	Glu	Asp	Lys	Asp	Ser	Pro	Phe	20	25	30	
Gly	Asn	Gly	Gln	Ser	Asn	Phe	Ser	Glu	Pro	Leu	Asn	Gly	Cys	Thr	Met	35	40	45	
Gln	Leu	Ser	Thr	Val	Ser	Gly	Thr	Ser	Gln	Asn	Ala	Tyr	Gly	Gln	Asp	50	55	60	
Ser	Pro	Ser	Cys	Tyr	Ile	Pro	Leu	Arg	Arg	Leu	Gln	Asp	Leu	Ala	Ser	65	70	75	80
Met	Ile	Asn	Val	Glu	Tyr	Leu	Asn	Gly	Ser	Ala	Asp	Gly	Ser	Glu	Ser	85	90	95	
Phe	Gln	Asp	Pro	Glu	Lys	Ser	Asp	Ser	Arg	Ala	Gln	Thr	Pro	Ile	Val	100	105	110	
Cys	Thr	Ser	Leu	Ser	Pro	Gly	Gly	Pro	Thr	Ala	Leu	Ala	Met	Lys	Gln	115	120	125	
Glu	Pro	Ser	Cys	Asn	Asn	Ser	Pro	Glu	Leu	Gln	Val	Lys	Val	Thr	Lys	130	135	140	
Thr	Ile	Lys	Asn	Gly	Phe	Leu	His	Phe	Glu	Asn	Phe	Thr	Cys	Val	Asp	145	150	155	160
Asp	Ala	Asp	Val	Asp	Ser	Glu	Met	Asp	Pro	Glu	Gln	Pro	Val	Thr	Glu	165	170	175	
Asp	Glu	Ser	Ile	Glu	Glu	Ile	Phe	Glu	Glu	Thr	Gln	Thr	Asn	Ala	Thr	180	185	190	
Cys	Asn	Tyr	Glu	Thr	Lys	Ser	Glu	Asn	Gly	Val	Lys	Val	Ala	Met	Gly	195	200	205	
Ser	Glu	Gln	Asp	Ser	Thr	Pro	Glu	Ser	Arg	His	Gly	Ala	Val	Lys	Ser	210	215	220	
Pro	Phe	Leu	Pro	Leu	Ala	Pro	Gln	Thr	Glu	Thr	Gln	Lys	Asn	Lys	Gln	225	230	235	240
Arg	Asn	Glu	Val	Asp	Gly	Ser	Asn	Glu	Lys	Ala	Ala	Leu	Leu	Pro	Ala	245	250	255	
Pro	Phe	Ser	Leu	Gly	Asp	Thr	Asn	Ile	Thr	Ile	Glu	Glu	Gln	Leu	Asn	260	265	270	
Ser	Ile	Asn	Leu	Ser	Phe	Gln	Asp	Asp	Pro	Asp	Ser	Ser	Thr	Ser	Thr	275	280	285	
Leu	Gly	Asn	Met	Leu	Glu	Leu	Pro	Gly	Thr	Ser	Ser	Ser	Ser	Thr	Ser	290	295	300	
Gln	Glu	Leu	Pro	Phe	Cys	Gln	Pro	Lys	Lys	Lys	Ser	Thr	Pro	Leu	Lys	305	310	315	320
Tyr	Glu	Val	Gly	Asp	Leu	Ile	Trp	Ala	Lys	Phe	Lys	Arg	Arg	Pro	Trp	325	330	335	
Trp	Pro	Cys	Arg	Ile	Cys	Ser	Asp	Pro	Leu	Ile	Asn	Thr	His	Ser	Lys	340	345	350	
Met	Lys	Val	Ser	Asn	Arg	Arg	Pro	Tyr	Arg	Gln	Tyr	Tyr	Val	Glu	Ala	355	360	365	
Phe	Gly	Asp	Pro	Ser	Glu	Arg	Ala	Trp	Val	Ala	Gly	Lys	Ala	Ile	Val	370	375	380	
Met	Phe	Glu	Gly	Arg	His	Gln	Phe	Glu	Glu	Leu	Pro	Val	Leu	Arg	Arg	385	390	395	400
Arg	Gly	Lys	Gln	Lys	Glu	Lys	Gly	Tyr	Arg	His	Lys	Val	Pro	Gln	Lys	405	410	415	
Ile	Leu	Ser	Lys	Trp	Glu	Ala	Ser	Val	Gly	Leu	Ala	Glu	Gln	Tyr	Asp	420	425	430	
Val	Pro	Lys	Gly	Ser	Lys	Asn	Arg	Lys	Cys	Ile	Pro	Gly	Ser	Ile	Lys	435	440	445	

Leu	Asp	Ser	Glu	Glu	Asp	Met	Pro	Phe	Glu	Asp	Cys	Thr	Asn	Asp	Pro
450						455					460				
Glu	Ser	Glu	His	Asp	Leu	Leu	Leu	Asn	Gly	Cys	Leu	Lys	Ser	Leu	Ala
465					470					475					480
Phe	Asp	Ser	Glu	His	Ser	Ala	Asp	Glu	Lys	Glu	Lys	Pro	Cys	Ala	Lys
				485					490					495	
Ser	Arg	Ala	Arg	Lys	Ser	Ser	Asp	Asn	Pro	Lys	Arg	Thr	Ser	Val	Lys
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Lys	Gly	His	Ile	Gln	Phe	Glu	Ala	His	Lys	Asp	Glu	Arg	Arg	Gly	Lys
		515					520					525			
Ile	Pro	Glu	Asn	Leu	Gly	Leu	Asn	Phe	Ile	Ser	Gly	Asp	Ile	Ser	Asp
	530					535					540				
Thr	Gln	Ala	Ser	Asn	Glu	Leu	Ser	Arg	Ile	Ala	Asn	Ser	Leu	Thr	Gly
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Ser	Asn	Thr	Ala	Pro	Gly	Ser	Phe	Leu	Phe	Ser	Ser	Cys	Gly	Lys	Asn
				565					570					575	
Thr	Ala	Lys	Lys	Glu	Phe	Glu	Thr	Ser	Asn	Gly	Asp	Ser	Leu	Leu	Gly
				580				585					590		
Leu	Pro	Glu	Gly	Ala	Leu	Ile	Ser	Lys	Cys	Ser	Arg	Glu	Lys	Asn	Lys
		595					600					605			
Pro	Gln	Arg	Ser	Leu	Val	Cys	Gly	Ser	Lys	Val	Lys	Leu	Cys	Tyr	Ile
	610					615					620				
Gly	Ala	Gly	Asp	Glu	Glu	Lys	Arg	Ser	Asp	Ser	Ile	Ser	Ile	Cys	Thr
625					630					635					640
Thr	Ser	Asp	Asp	Gly	Ser	Ser	Asp	Leu	Asp	Pro	Ile	Glu	His	Ser	Ser
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Glu	Ser	Asp	Asn	Ser	Val	Leu	Glu	Ile	Pro	Asp	Ala	Phe	Asp	Arg	Thr
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Glu	Asn	Met	Leu	Ser	Met	Gln	Lys	Asn	Glu	Lys	Ile	Lys	Tyr	Ser	Arg
		675					680					685			
Phe	Ala	Ala	Thr	Asn	Thr	Arg	Val	Lys	Ala	Lys	Gln	Lys	Pro	Leu	Ile
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Lys	Gly	Gly	Ala	Ala	Asn	Gln	Ala	Leu	Leu	His	Ser	Lys	Ser	Lys	Gln
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		915					920						925		

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 Lys Lys Gly Asp Leu Gly Leu Ser Lys Lys Cys Tyr Glu Ala Gly His  
 1425 1430 1435 1440  
 Leu Glu Asn Gly Ile Thr Glu Ser Cys Ala Thr Ser Tyr Ser Lys Asp  
 1445 1450 1455  
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 1460 1465 1470  
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 His Arg Thr Ala Thr Ser Pro Lys Glu Thr Val Glu Glu Gly Val Glu  
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 1585 1590 1595 1600  
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 Phe Arg Cys Ser Leu His Ile Cys Ile Thr Cys His Ala Ala Asn Pro  
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 Ala Asn Val Ser Ala Ser Lys Gly Arg Leu Met Arg Cys Val Arg Cys  
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 Trp Val Lys Val Gly Arg Tyr Arg Trp Trp Pro Ala Glu Ile Cys His  
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 1875 1880 1885

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 Cys Gly Ile Asp Ser Glu Cys Ile Asn Arg Met Leu Leu Tyr Glu Cys  
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 1925 1930 1935  
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 Gly Trp Gly Leu Arg Thr Lys Thr Asp Ile Lys Lys Gly Glu Phe Val  
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 1985 1990 1995 2000  
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 2005 2010 2015  
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&lt;210&gt; 37

&lt;211&gt; 8431

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
 synthetic construct

&lt;400&gt; 37

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&lt;210&gt; 38

&lt;211&gt; 1784

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 38

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 35          40          45
Ala Ser Pro His Ile Gly Arg Ser Asn Glu Glu Glu Glu Thr Ser Asp
 50          55          60
Ser Ser Leu Glu Lys Gln Thr Arg Ser Lys Tyr Cys Thr Glu Thr Ser
 65          70          75          80
Gly Val His Gly Asp Ser Pro Tyr Gly Ser Gly Thr Met Asp Thr His
 85          90          95
Ser Leu Glu Ser Lys Ala Glu Arg Ile Ala Arg Tyr Lys Ala Glu Arg
100          105          110
Arg Arg Gln Leu Ala Glu Lys Tyr Gly Leu Thr Leu Asp Pro Glu Ala
115          120          125
Asp Ser Glu Tyr Leu Ser Arg Tyr Thr Lys Ser Arg Lys Glu Pro Asp
130          135          140
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145          150          155          160
Arg Asp Ala Ser Ser Leu Tyr Pro Gly Thr Glu Thr Met Gly Leu Arg
165          170          175
Thr Cys Ala Gly Glu Ser Lys Asp Tyr Ala Leu His Ala Gly Asp Gly
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Ser Ser Asp Pro Glu Val Leu Leu Asn Ile Glu Asn Gln Arg Arg Gly
195          200          205
Gln Glu Leu Ser Ala Thr Arg Gln Ala His Asp Leu Ser Pro Ala Ala
210          215          220
Glu Ser Ser Ser Thr Phe Ser Phe Ser Gly Arg Asp Ser Ser Phe Thr
225          230          235          240
Glu Val Pro Arg Ser Pro Lys His Ala His Ser Ser Ser Leu Gln Gln
245          250          255
Ala Ala Ser Arg Ser Pro Ser Phe Gly Asp Pro Gln Leu Ser Pro Glu
260          265          270
Ala Arg Pro Arg Cys Thr Ser His Ser Glu Thr Pro Thr Val Asp Asp
275          280          285

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Glu	Glu	Lys	Val	Asp	Glu	Arg	Ala	Lys	Leu	Ser	Val	Ala	Ala	Lys	Arg
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Leu	Leu	Phe	Arg	Glu	Met	Glu	Lys	Ser	Phe	Asp	Glu	Gln	Asn	Val	Pro
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Lys	Arg	Arg	Ser	Arg	Asn	Thr	Ala	Val	Glu	Gln	Arg	Leu	Arg	Arg	Leu
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Gln	Asp	Arg	Ser	Leu	Thr	Gln	Pro	Ile	Thr	Thr	Glu	Glu	Val	Val	Ile
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Gln	Thr	Asn	Glu	Gly	Lys	Glu	Leu	Ala	Glu	Gln	Gly	Glu	Pro	Asp	Ser
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Ser	Thr	Leu	Ser	Leu	Ala	Glu	Lys	Leu	Ala	Leu	Phe	Asn	Lys	Leu	Ser
385					390					395					400
Gln	Pro	Val	Ser	Lys	Ala	Ile	Ser	Thr	Arg	Asn	Arg	Ile	Asp	Thr	Arg
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Gln	Arg	Arg	Met	Asn	Ala	Arg	Tyr	Gln	Thr	Gln	Pro	Val	Thr	Leu	Gly
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Glu	Val	Glu	Gln	Val	Gln	Ser	Gly	Lys	Leu	Ile	Pro	Phe	Ser	Pro	Ala
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Glu	Asn	Lys	Gly	Met	Leu	Arg	Glu	Tyr	Gly	Glu	Thr	Glu	Ser	Lys	Arg
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Ala	Leu	Thr	Gly	Arg	Asp	Ser	Gly	Met	Glu	Lys	Tyr	Gly	Ser	Phe	Glu
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Glu	Ala	Glu	Ala	Ser	Tyr	Pro	Ile	Leu	Asn	Arg	Ala	Arg	Glu	Gly	Asp
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Ser	His	Lys	Glu	Ser	Lys	Tyr	Ala	Val	Pro	Arg	Arg	Gly	Ser	Leu	Glu
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Arg	Ala	Asn	Pro	Ile	Thr	His	Leu	Gly	Asp	Glu	Pro	Lys	Glu	Phe	
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Ser	Met	Ala	Lys	Met	Asn	Ala	Gln	Gly	Asn	Leu	Asp	Leu	Arg	Asp	Arg
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Phe	Ser	Leu	Arg	Ala	Ala	Glu	Phe	Gly	Glu	Pro	Thr	Ser	Glu	Gln	Thr
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Asn	Cys	Ile	Tyr	Arg	Leu	Met	Asp	Asp	Lys	Leu	Val	Pro	Asp	Asp	Asp	1140	1145	1150
Tyr	Trp	Gly	Lys	Ile	Pro	Lys	Cys	Ser	Leu	Leu	Gln	Pro	Lys	Glu	Val	1155	1160	1165
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<223> Description of Artificial Sequence:/note =  
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taccgctgg	ccagacctcct	ggccaggcca	ctcccggagg	gggtcgatcc	tctgaaagctt	5700
gagatctatc	tcaccgacga	agacttcgag	tttgactag	acatgacgag	ggatgaatac	5760
aacgcctgc	ccgcctggaa	gcaggtgaac	ctgaagaaag	caaaaggcct	gttctgagtg	5820
gggagacgcc	agaggagcct	cacggtcacg	tccaacaaca	ccactgcacc	agggaaatgg	5880
atatatatatt	ttggactggt	gtttttcaca	aagtattttt	caatcagagt	tttcagaacc	5940
tgacattggt	aaagatactg	cttgtcccgg	agttgtgtat	tttgtaaagt	ttcaagggaa	6000
ctgtttggaa	acttctttcc	accattcagg	aggttatcag	aattaataaa	agtatctggt	6060
atgtgcactt	aagccgcagc	tgctatagat	agcactgcct	tcttggtcca	gctaggcaat	6120
gccttttttt	ttttttttga	agcagttctc	tttataaagt	gttattttga	tagtttgtgg	6180

```

attctaaaaat atatatatat ttatataaac accatataag tcaaatatgt atttaacaaa 6240
gcaatatgta ttcatttcaact ttcaagattt gtttttggtgt caaaataaca tgaaaaggta 6300
gatggagttg cttctgttga attagctctg ccaccaatat gtatcttcat acacgtttgg 6360
aaatgtttcc tgcagcatta ggtatgactt gttctgagta ctgcttccgg tgctaaaatg 6420
aacaaagaat ttgtacttaa tggcatggac tctggagaat ctatgcgaat caacctttct 6480
accttaatat ctccccaaaa atgtatagtg ccttggtttt atgtacagtt tatatacaga 6540
aaagtttgct ctgcattttt gatgatgggt tggaacatta tctacaattt tactctcaaa 6600
tagtcaaaat aaaaacatct caatttctaa taccggttgt aaacaaacag tacacatgtc 6660
attttgtgat ataggactcc caaataaaag tatcagaata aacacaacaa ttaactggt 6719

```

&lt;210&gt; 40

&lt;211&gt; 731

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 40

```

Met Val Val Glu His Pro Glu Phe Leu Lys Ala Gly Lys Glu Pro Gly
 1          5          10          15
Leu Gln Ile Trp Arg Val Glu Lys Phe Asp Leu Val Pro Val Pro Pro
 20          25          30
Asn Leu Tyr Gly Asp Phe Phe Thr Gly Asp Ala Tyr Val Ile Leu Lys
 35          40          45
Thr Val Gln Leu Arg Asn Gly Asn Leu Gln Tyr Asp Leu His Tyr Trp
 50          55          60
Leu Gly Asn Glu Cys Ser Gln Asp Glu Ser Gly Ala Ala Ala Ile Phe
 65          70          75          80
Thr Val Gln Leu Asp Asp Tyr Leu Asn Gly Arg Ala Val Gln His Arg
 85          90          95
Glu Val Gln Gly Phe Glu Ser Ser Thr Phe Ser Gly Tyr Phe Lys Ser
100          105          110
Gly Leu Lys Tyr Lys Lys Gly Gly Val Ala Ser Gly Phe Lys His Val
115          120          125
Val Pro Asn Glu Val Val Val Gln Arg Leu Phe Gln Val Lys Gly Arg
130          135          140
Arg Val Val Arg Ala Thr Glu Val Pro Val Ser Trp Asp Ser Phe Asn
145          150          155          160
Asn Gly Asp Cys Phe Ile Leu Asp Leu Gly Asn Asn Ile Tyr Gln Trp
165          170          175
Cys Gly Ser Gly Ser Asn Lys Phe Glu Arg Leu Lys Ala Thr Gln Val
180          185          190
Ser Lys Gly Ile Arg Asp Asn Glu Arg Ser Gly Arg Ala Gln Val His
195          200          205
Val Ser Glu Glu Glu Thr Glu Pro Glu Ala Met Leu Gln Val Leu Gly
210          215          220
Pro Lys Pro Ala Leu Pro Glu Gly Thr Glu Asp Thr Ala Lys Glu Asp
225          230          235          240
Ala Ala Asn Arg Lys Leu Ala Lys Leu Tyr Lys Val Ser Asn Gly Ala
245          250          255
Gly Ser Met Ser Val Ser Leu Val Ala Asp Glu Asn Pro Phe Ala Gln
260          265          270
Gly Pro Leu Arg Ser Glu Asp Cys Phe Ile Leu Asp His Gly Arg Asp
275          280          285
Gly Lys Ile Phe Val Trp Lys Gly Lys Gln Ala Asn Met Glu Glu Arg
290          295          300

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Lys	Ala	Ala	Leu	Lys	Thr	Ala	Ser	Asp	Phe	Ile	Ser	Lys	Met	Gln	Tyr	305	310	315	320
Pro	Arg	Gln	Thr	Gln	Val	Ser	Val	Leu	Pro	Glu	Gly	Gly	Glu	Thr	Pro	325	330	335	
Leu	Phe	Lys	Gln	Phe	Phe	Lys	Asn	Trp	Arg	Asp	Pro	Asp	Gln	Thr	Asp	340	345	350	
Gly	Pro	Gly	Leu	Gly	Tyr	Leu	Ser	Ser	His	Ile	Ala	Asn	Val	Glu	Arg	355	360	365	
Val	Pro	Phe	Asp	Ala	Gly	Thr	Leu	His	Thr	Ser	Thr	Ala	Met	Ala	Ala	370	375	380	
Gln	His	Gly	Met	Asp	Asp	Gly	Thr	Gly	Gln	Lys	Gln	Ile	Trp	Arg		385	390	395	400
Ile	Glu	Gly	Ser	Asn	Lys	Val	Pro	Val	Asp	Pro	Ala	Thr	Tyr	Gly	Gln	405	410	415	
Phe	Tyr	Gly	Gly	Asp	Ser	Tyr	Ile	Ile	Leu	Tyr	Asn	Tyr	Arg	His	Gly	420	425	430	
Gly	Arg	Gln	Gly	Gln	Ile	Ile	Tyr	Asn	Trp	Gln	Gly	Ala	Gln	Ser	Thr	435	440	445	
Gln	Asp	Glu	Val	Ala	Ala	Ser	Ala	Ile	Leu	Thr	Ala	Gln	Leu	Asp	Glu	450	455	460	
Glu	Leu	Gly	Gly	Thr	Pro	Val	Gln	Ser	Arg	Val	Val	Gln	Gly	Lys	Glu	465	470	475	480
Pro	Ala	His	Leu	Met	Ser	Leu	Phe	Gly	Gly	Lys	Pro	Met	Ile	Ile	Tyr	485	490	495	
Lys	Gly	Gly	Thr	Ser	Arg	Asp	Gly	Gly	Gln	Thr	Ala	Pro	Ala	Ser	Ile	500	505	510	
Arg	Leu	Phe	Gln	Val	Arg	Ala	Ser	Ser	Ser	Gly	Ala	Thr	Arg	Ala	Val	515	520	525	
Glu	Val	Met	Pro	Lys	Ser	Gly	Ala	Leu	Asn	Ser	Asn	Asp	Ala	Phe	Val	530	535	540	
Leu	Lys	Thr	Pro	Ser	Ala	Ala	Tyr	Leu	Trp	Val	Gly	Ala	Gly	Ala	Ser	545	550	555	560
Glu	Ala	Glu	Lys	Thr	Ala	Ala	Gln	Glu	Leu	Leu	Lys	Val	Leu	Arg	Ser	565	570	575	
Gln	His	Val	Gln	Val	Glu	Glu	Gly	Ser	Glu	Pro	Asp	Gly	Phe	Trp	Glu	580	585	590	
Ala	Leu	Gly	Gly	Lys	Thr	Ser	Tyr	Arg	Thr	Ser	Pro	Arg	Leu	Lys	Asp	595	600	605	
Lys	Lys	Met	Asp	Ala	His	Pro	Pro	Arg	Leu	Phe	Ala	Cys	Ser	Asn	Arg	610	615	620	
Ile	Gly	Arg	Phe	Val	Ile	Glu	Glu	Val	Pro	Gly	Glu	Leu	Met	Gln	Glu	625	630	635	640
Asp	Leu	Ala	Thr	Asp	Val	Met	Leu	Leu	Asp	Thr	Trp	Asp	Gln	Val		645	650	655	
Phe	Val	Trp	Val	Gly	Lys	Asp	Ser	Gln	Glu	Glu	Lys	Thr	Glu	Ala		660	665	670	
Leu	Thr	Ser	Ala	Lys	Arg	Tyr	Ile	Glu	Thr	Asp	Pro	Ala	Asn	Arg	Asp	675	680	685	
Arg	Arg	Thr	Pro	Ile	Thr	Val	Val	Arg	Gln	Gly	Phe	Glu	Pro	Pro	Ser	690	695	700	
Phe	Val	Gly	Trp	Phe	Leu	Gly	Trp	Asp	Asn	Asn	Tyr	Trp	Ser	Val	Asp	705	710	715	720
Pro	Leu	Asp	Arg	Ala	Leu	Ala	Glu	Leu	Ala	Ala						725	730		

&lt;210&gt; 41

&lt;211&gt; 2447

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 41

tgagcgcggc	ccagcactat	ggtggtggag	caccccgaa	tctgaaggc	aggggaaggag	60
cctggcctgc	agatctggcg	tgtggagaag	tttgacctgg	tgctgtgcc	ccccaacctc	120
tatggagact	tcttcacggg	tgatgcctat	gtcatcctga	agactgtgca	gctgaggaat	180
gggaatctgc	agtatgacct	ccactatttg	ctgggcaatg	aatgcagcca	ggatgagagc	240
ggggctgctg	ccatctttac	tgtgcaactg	gatgactacc	tgaacggccg	ggctgtgcag	300
caccgtgagg	ttcagggtct	tgatgcgtcc	accttctccg	gctacttcaa	gtctggactt	360
aagtacaaga	aaggagggtg	ggcatctgga	ttcaaacacg	tggtacccaa	tgagggtggtg	420
gtccagaggc	tcttccaggt	caaaggacgc	ctgtgtagtc	gtgctactga	ggtacctgtg	480
tctggggaca	gtttcaacaa	tggcgactgc	ttcattctgg	acctgggaaa	caatatctat	540
cagtgggtgtg	gctctggcag	caacaaattt	gaaaggctga	aggccacaca	ggtgtccaag	600
ggcatccggg	acaacgagag	gagtggccgt	gctcaagtag	acgtgtctga	agaggagact	660
gagcccgagg	cgatgctgca	ggtgctgggc	cccaagccgg	ctctgcctga	aggtaccgag	720
gacacagcca	aggaagatgc	agccaaccgc	aagctggcca	agctctacaa	ggtctccaac	780
ggtgcaggta	gcatgtcagt	ctccctagt	gctgatgaga	accccttcgc	ccagggggccc	840
ctgagatctg	aggactgctt	catcctggac	catggcagag	atgggaaaat	ctttgttttg	900
aaaggcaagc	aggccaacat	ggaggagcgg	aaggctgccc	tcaaaacagc	ctctgacttc	960
atctccaaga	tgcagtaccc	caggcagacc	caggtttcag	ttctcccaga	gggcgggtgag	1020
acccctctct	ttaagcagtt	cttcaagaac	tggcgggacc	cagaccagac	agatggcccc	1080
ggcctgggct	acctctccag	ccacattgcc	aacgtggagc	gcgtaccttt	cgatgccggc	1140
acgtgcaca	cctccaccgc	catggccgct	cagcacggca	tggatgatga	tggaaactggc	1200
cagaaacaga	tctggagaat	tgaagggttc	aacaagggtg	cagtggaccc	tgccacatac	1260
ggacagttct	atggaggcga	cagctacatc	attctgtaca	actaccgcca	cgggtggccgc	1320
cagggaacaga	tcactacaaa	ctggcagggt	gtcagctcta	cccaggatga	ggttgctgct	1380
tctgccatcc	tgactgccc	gctggatgag	gagctgggag	gaactcctgt	ccagagccga	1440
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ggcggaaga	cgctctaccg	cacatccccc	aggcttaagg	acaagaagat	ggatgcccac	1860
cctcctcgac	tctttgcctg	ctccaacagg	atcggacgct	ttgtgatcga	agaggttcct	1920
ggcgagctta	tgcaggaaga	cctggctact	gatgacgtca	tgctcctgga	cacctgggac	1980
cagggtcttg	tctgggttg	aaaagactcc	caggaagaag	aaaagacgga	agccttgact	2040
tctgctaagc	ggtacatcga	gacagatcca	gcaaatcggg	acaggcggac	ccccatcaca	2100
gtcgttaggc	agggtcttga	gcctccttcc	ttcgtgggct	ggttcctcgg	ctgggacaac	2160
aactactggt	cggtggatcc	tttggaccgg	gccttggctg	agctggctgc	ctgagtaagg	2220
accaagccat	caatgtcacc	aatcagtgcc	tttgagggtt	gtccatctcc	caaagacatc	2280
atatggcaag	caggaaaact	atgatgtgtg	cgcgctgtt	tttgtttttg	ttttttacgg	2340
tagccaaaac	aagcccttgt	ggaaactcag	ggtctttaca	gaattgcttc	aaatgtctgt	2400
actttggaaa	tgaagccaa	taaaagcttt	ttgaagtga	aaaaaaa		2447

<210> 42

<211> 928

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 42

Met	Pro	Pro	Lys	Thr	Pro	Arg	Lys	Thr	Ala	Ala	Thr	Ala	Ala	Ala	Ala
1				5				10					15		
Ala	Ala	Glu	Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Glu	Glu	Asp	
			20					25					30		

Pro	Glu	Gln	Asp	Ser	Gly	Pro	Glu	Asp	Leu	Pro	Leu	Val	Arg	Leu	Glu
		35					40					45			
Phe	Glu	Glu	Thr	Glu	Glu	Pro	Asp	Phe	Thr	Ala	Leu	Cys	Gln	Lys	Leu
	50					55					60				
Lys	Ile	Pro	Asp	His	Val	Arg	Glu	Arg	Ala	Trp	Leu	Thr	Trp	Glu	Lys
65					70					75					80
Val	Ser	Ser	Val	Asp	Gly	Val	Leu	Gly	Gly	Tyr	Ile	Gln	Lys	Lys	Lys
				85					90					95	
Glu	Leu	Trp	Gly	Ile	Cys	Ile	Phe	Ile	Ala	Ala	Val	Asp	Leu	Asp	Glu
			100					105					110		
Met	Ser	Phe	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	Ile	Glu	Ile	Ser	Val
		115					120					125			
His	Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	Thr	Ser	Thr	Lys	Val
	130					135					140				
Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe	Ala
145					150					155					160
Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	Gln
				165					170					175	
Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	Lys
			180					185					190		
Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met
		195					200					205			
Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp
	210					215					220				
Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys
225					230					235					240
Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	Gly
				245					250					255	
Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg
			260					265					270		
Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val
		275					280					285			
Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	Gly
	290					295					300				
Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg
305					310					315					320
Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe
				325					330					335	
Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu
			340					345					350		
Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val
			355				360						365		
Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln
	370					375					380				
Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu
385					390					395					400
Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu
				405					410					415	
Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys
			420					425					430		
Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu
		435					440					445			
Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu
	450					455					460				
Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn
465					470					475					480
Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala
				485					490					495	
Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu
			500					505					510		

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Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe
   515           520           525
Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg
   530           535           540
Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser
  545           550           555           560
Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser
   565           570           575
Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu
   580           585           590
Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser
   595           600           605
Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser
   610           615           620
Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys
  625           630           635           640
Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg
   645           650           655
Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu
   660           665           670
His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu
   675           680           685
Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met
   690           695           700
Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys
  705           710           715           720
Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln
   725           730           735
Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile
   740           745           750
Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile
   755           760           765
Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His
   770           775           780
Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro
  785           790           795           800
Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser
   805           810           815
Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu
   820           825           830
Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile
   835           840           845
Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu
   850           855           860
Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu
  865           870           875           880
Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys
   885           890           895
Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln
   900           905           910
Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys
   915           920           925

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&lt;210&gt; 43

&lt;211&gt; 2994

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: /note =  
synthetic construct



&lt;400&gt; 43

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ccgccgcgga	aaggcgcat	gccgcccaaa	acccccgaa	aaacggccgc	caccgccgcc	180
gctgccgccg	cggaaccccc	ggcaccgccg	ccgccgcccc	ctcctgagga	ggaccagag	240
caggacagcg	gcccggagga	cctgcctctc	gtcaggcttg	agtttgaaga	aacagaagaa	300
cctgattttt	ctgcattatg	tcagaaatta	aagataccag	atcatgtcag	agagagagct	360
tggttaaact	gggagaaagt	ttcatctgtg	gatggagtat	tgggaggtta	tattcaaaag	420
aaaaaggaac	tgtggggaat	ctgtatcttt	attgcagcag	ttgacctaga	tgagatgtcg	480
ttcactttta	ctgagctaca	gaaaaacata	gaaatcagtg	tccataaaatt	ctttaactta	540
ctaaaagaaa	ttgataccag	taccaaagtt	gataatgcta	tgtcaagact	gttgaagaag	600
tatgatgtat	tgtttgcact	cttcagcaaa	ttggaaagga	catgtgaact	tatatatttg	660
acacaaccca	gcagttcgat	atctactgaa	ataaattctg	cattggtgct	aaaagtttct	720
tggatcacat	ttttattagc	taaaggggaa	gtattacaaa	tggaaagatga	tctggtgatt	780
tcattttcagt	taatgctatg	tgtccttgac	tattttatta	aactctcacc	tcccatgttg	840
ctcaaagaac	catataaaaac	agctgttata	cccattaatg	gttcacctcg	aacaccagg	900
cgaggtcaga	acaggagtgc	acggatagca	aaacaactag	aaaatgatac	agaatttatt	960
gaagttctct	gtaaagaaca	tgaatgtaat	atagatgag	tgaaaaatgt	ttatttcaaa	1020
aattttatatac	cttttatgaa	ttctcttgga	cttgtaacat	ctaattggact	tccagaggtt	1080
gaaaatcttt	ctaaacgata	cgaagaaatt	tatcttaaaa	ataaagatct	agatgcaaga	1140
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caaccttcag	aaaatctgat	ttcctatttt	aacaactgca	cagtgaatcc	aaaagaaagt	1380
atactgaaaa	gagtgaagga	tataggatac	atcttttaaag	agaaatttgc	taaagctgtg	1440
ggacagggtt	gtgtcgaaat	tggatcacag	cgatacaaac	ttggagttcg	cttgtattac	1500
cgagtaatgg	aatccatgct	taaatcagaa	gaagaacgat	tatccattca	aaatttttagc	1560
aaacttctga	atgacaacat	ttttcatatg	tctttatttg	cgtgcgctct	tgaggttgta	1620
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ccatggattc	tgaatgtgct	taatttaaaa	gcctttgatt	tttaciaaagt	gatcgaaagt	1740
tttatcaaag	cagaaggcaa	cttgacaaga	gaaatgataa	aacattttaga	acgatgtgaa	1800
catcgaaatca	tggaaatccct	tgcattggctc	tcagattcac	ctttatttga	tcttattaaa	1860
caatcaaagg	accgagaagg	accaactgat	caccttgaat	ctgcttgctc	tcttaattctt	1920
cctctccaga	ataatcacac	tgcagcagat	atgtatcttt	ctcctgtaag	atctccaaag	1980
aaaaaagggt	caactacgcg	tgtaaattct	actgcaaagt	cagagacaca	agcaacctca	2040
gccttccaga	cccagaagcc	attgaaatct	acctctcttt	cactgtttta	taaaaaagtg	2100
tatcggttag	cctatctccg	gctaaataca	ctttgtgaac	gccttctgtc	tgagcaccac	2160
gaattagaac	atatcatctg	gacctttttc	cagcacaccc	tgcagaatga	gtatgaactc	2220
atgagagaca	ggcattttgga	ccaaattatg	atgtgttcca	tgtatggcat	atgcaaagtg	2280
agaatatatag	accttaaat	caaaatcatt	gtaacagcat	acaaggatct	tcctcatgct	2340
gttcaggaga	cattcaaacg	tgttttgatc	aaagaagagg	agtatgattc	tattatagta	2400
ttctataact	cggctcttc	gcagagactg	aaaacaaata	ttttgcagta	tgcttccacc	2460
aggcccccta	ccttgtcacc	aatacctcac	attcctcgaa	gcccttacia	gtttcctagt	2520
tcacctttac	ggattcctgg	aggaacatc	tatatctcac	ccctgaagag	tccatataaa	2580
atttcagaag	gtctgccaac	accaacaaaa	atgactccaa	gatcaagaat	cttagtatca	2640
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agcgaccgtg	tgtcmetaag	aagtgttgaa	ggaagcaacc	ctcctaaacc	actgaaaaaa	2760
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tccaaatttc	agcagaaact	ggcagaaatg	acttctactc	gaacacgaat	gcaaaagcag	2880
aaaatgaatg	atagcatgga	tacctcaaac	aaggaagaga	aatgaggatc	tcaggacctt	2940
ggtggacact	gtgtacacct	ctggattcat	tgtctctcac	agatgtgact	gtat	2994

&lt;210&gt; 44

&lt;211&gt; 782

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: /note =  
synthetic construct

&lt;400&gt; 44

```

      .
Met Ala Pro His Arg Pro Ala Pro Ala Leu Leu Cys Ala Leu Ser Leu
 1      5      10      15
Ala Leu Cys Ala Leu Ser Leu Pro Val Arg Ala Ala Thr Ala Ser Arg
 20      25      30
Gly Ala Ser Gln Ala Gly Ala Pro Gln Gly Arg Val Pro Glu Ala Arg
 35      40      45
Pro Asn Ser Met Val Val Glu His Pro Glu Phe Leu Lys Ala Gly Lys
 50      55      60
Glu Pro Gly Leu Gln Ile Trp Arg Val Glu Lys Phe Asp Leu Val Pro
 65      70      75      80
Val Pro Thr Asn Leu Tyr Gly Asp Phe Phe Thr Gly Asp Ala Tyr Val
 85      90      95
Ile Leu Lys Thr Val Gln Leu Arg Asn Gly Asn Leu Gln Tyr Asp Leu
 100     105     110
His Tyr Trp Leu Gly Asn Glu Cys Ser Gln Asp Glu Ser Gly Ala Ala
 115     120     125
Ala Ile Phe Thr Val Gln Leu Asp Asp Tyr Leu Asn Gly Arg Ala Val
 130     135     140
Gln His Arg Glu Val Gln Gly Phe Glu Ser Ala Thr Phe Leu Gly Tyr
 145     150     155     160
Phe Lys Ser Gly Leu Lys Tyr Lys Lys Gly Gly Val Ala Ser Gly Phe
 165     170     175
Lys His Val Val Pro Asn Glu Val Val Val Gln Arg Leu Phe Gln Val
 180     185     190
Lys Gly Arg Arg Val Val Arg Ala Thr Glu Val Pro Val Ser Trp Glu
 195     200     205
Ser Phe Asn Asn Gly Asp Cys Phe Ile Leu Asp Leu Gly Asn Asn Ile
 210     215     220
His Gln Trp Cys Gly Ser Asn Ser Asn Arg Tyr Glu Arg Leu Lys Ala
 225     230     235     240
Thr Gln Val Ser Lys Gly Ile Arg Asp Asn Glu Arg Ser Gly Arg Ala
 245     250     255
Arg Val His Val Ser Glu Glu Gly Thr Glu Pro Glu Ala Met Leu Gln
 260     265     270
Val Leu Gly Pro Lys Pro Ala Leu Pro Ala Gly Thr Glu Asp Thr Ala
 275     280     285
Lys Glu Asp Ala Ala Asn Arg Lys Leu Ala Lys Leu Tyr Lys Val Ser
 290     295     300
Asn Gly Ala Gly Thr Met Ser Val Ser Leu Val Ala Asp Glu Asn Pro
 305     310     315     320
Phe Ala Gln Gly Ala Leu Lys Ser Glu Asp Cys Phe Ile Leu Asp His
 325     330     335
Gly Lys Asp Gly Lys Ile Phe Val Trp Lys Gly Lys Gln Ala Asn Thr
 340     345     350
Glu Glu Arg Lys Ala Ala Leu Lys Thr Ala Ser Asp Phe Ile Thr Lys
 355     360     365
Met Asp Tyr Pro Lys Gln Thr Gln Val Ser Val Leu Pro Glu Gly Gly
 370     375     380
Glu Thr Pro Leu Phe Lys Gln Phe Phe Lys Asn Trp Arg Asp Pro Asp
 385     390     395     400
Gln Thr Asp Gly Leu Gly Leu Ser Tyr Leu Ser Ser His Ile Ala Asn
 405     410     415
Val Glu Arg Val Pro Phe Asp Ala Ala Thr Leu His Thr Ser Thr Ala
 420     425     430
Met Ala Ala Gln His Gly Met Asp Asp Asp Gly Thr Gly Gln Lys Gln
 435     440     445
Ile Trp Arg Ile Glu Gly Ser Asn Lys Val Pro Val Asp Pro Ala Thr
 450     455     460

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Tyr Gly Gln Phe Tyr Gly Gly Asp Ser Tyr Ile Ile Leu Tyr Asn Tyr  
 465 470 475 480  
 Arg His Gly Gly Arg Gln Gly Gln Ile Ile Tyr Asn Trp Gln Gly Ala  
 485 490 495  
 Gln Ser Thr Gln Asp Glu Val Ala Ala Ser Ala Ile Leu Thr Ala Gln  
 500 505 510  
 Leu Asp Glu Glu Leu Gly Gly Thr Pro Val Gln Ser Arg Val Val Gln  
 515 520 525  
 Gly Lys Glu Pro Ala His Leu Met Ser Leu Phe Gly Gly Lys Pro Met  
 530 535 540  
 Ile Ile Tyr Lys Gly Gly Thr Ser Arg Glu Gly Gly Gln Thr Ala Pro  
 545 550 555 560  
 Ala Ser Thr Arg Leu Phe Gln Val Arg Ala Asn Ser Ala Gly Ala Thr  
 565 570 575  
 Arg Ala Val Glu Val Leu Pro Lys Ala Gly Ala Leu Asn Ser Asn Asp  
 580 585 590  
 Ala Phe Val Leu Lys Thr Pro Ser Ala Ala Tyr Leu Trp Val Gly Thr  
 595 600 605  
 Gly Ala Ser Glu Ala Glu Lys Thr Gly Ala Gln Glu Leu Leu Arg Val  
 610 615 620  
 Leu Arg Ala Gln Pro Val Gln Val Ala Glu Gly Ser Glu Pro Asp Gly  
 625 630 635 640  
 Phe Trp Glu Ala Leu Gly Gly Lys Ala Ala Tyr Arg Thr Ser Pro Arg  
 645 650 655  
 Leu Lys Asp Lys Lys Met Asp Ala His Pro Pro Arg Leu Phe Ala Cys  
 660 665 670  
 Ser Asn Lys Ile Gly Arg Phe Val Ile Glu Glu Val Pro Gly Glu Leu  
 675 680 685  
 Met Gln Glu Asp Leu Ala Thr Asp Asp Val Met Leu Leu Asp Thr Trp  
 690 695 700  
 Asp Gln Val Phe Val Trp Val Gly Lys Asp Ser Gln Glu Glu Glu Lys  
 705 710 715 720  
 Thr Glu Ala Leu Thr Ser Ala Lys Arg Tyr Ile Glu Thr Asp Pro Ala  
 725 730 735  
 Asn Arg Asp Arg Arg Thr Pro Ile Thr Val Val Lys Gln Gly Phe Glu  
 740 745 750  
 Pro Pro Ser Phe Val Gly Trp Phe Leu Gly Trp Asp Asp Asp Tyr Trp  
 755 760 765  
 Ser Val Asp Pro Leu Asp Arg Ala Met Ala Glu Leu Ala Ala  
 770 775 780

&lt;210&gt; 45

&lt;211&gt; 2663

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
 synthetic construct

&lt;400&gt; 45

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gcgcgctgtc	gctgcccgtc	cgcgcggcca	ctgcgtcgcg	gggggcgtcc	caggcggggg	120
cgcccagg	gcgggtgccc	gaggcgcggc	ccaacagcat	ggtggtggaa	caccccgagt	180
tccctaaggc	agggaaggag	cctggcctgc	agatctggcg	tgtggagaag	ttcgatctgg	240
tgcccgtgcc	caccaacctt	tatggagact	tcttcacggg	cgacgcctac	gtcatcctga	300
agacagtgca	gctgaggaac	ggaaatctgc	agtatgacct	ccactactgg	ctgggcaatg	360
agtgcagcca	ggatgagagc	ggggcgggcg	ccatctttac	cgtgcagctg	gatgactacc	420
tgaacggccg	ggccgtgcag	caccgtgagg	tccagggctt	cgagtcggcc	accttcctag	480
gctacttcaa	gtctggcctg	aagtacaaga	aaggaggtgt	ggcatcagga	ttcaagcacg	540
tgttacccaa	cgaggtggtg	gtgcagagac	tcttcagggt	caaagggcgg	cgtgtggtcc	600

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gtgccaccga ggtacctgtg tctctgggaga gcttcaacaa tggcgactgc ttcctccttg 660
acctggggcaa caacatccac cagtgggtgtg gttccaacag caatcggtat gaaagactga 720
aggccacaca ggtgtccaag ggcattccggg acaacgagcg gagtggccgg gcccgagtgc 780
acgtgtctga ggagggcact gagcccgagg cgatgtctca ggtgtctggg cccaagccgg 840
ctctgcctgc aggtaccgag gacaccgcca aggaggatgc ggccaaccgc aagctggcca 900
agctctacaa ggtctccaat ggtgcaggga ccatgtccgt ctccctcgtg gctgatgaga 960
accccttcgc ccagggggcc ctgaagtcag aggactgctt catcctggac cacggcaaaag 1020
atgggaaaaat ctttgtcttg aaaggcaagc aggcaaacac ggaggagagg aaggctgccc 1080
tcaaaacagc ctctgacttc atcaccaaga tggactaccc caagcagact caggtctcgg 1140
tccttcctga gggcggtgag accccactgt tcaagcagtt cttcaagaac tggcgggacc 1200
cagaccagac agatggcctg ggcttgctct acctttccag ccataatcgcc aacgtggagc 1260
gggtgccctt cgacgcgcgc accctgcaca cctccactgc catggccgcc cagcacggca 1320
tggatgacga tggcacaggc cagaaacaga tctggagaat cgaaggttcc aacaaggtgc 1380
ccgtggaccc tgccacatat ggacagttct atggaggcga cagctacatc attctgtaca 1440
actaccgcca tgggtggcgc caggggcaga taatctataa ctggcagggg gccaggtcta 1500
cccaggatga ggtcgctgca tctgccatcc tgactgctca gctggatgag gagctgggag 1560
gtacccctgt ccagagccgt gtggtccaag gcaaggagcc cgcccacctc atgagcctgt 1620
ttggtgggaa gcccatgac atctacaagg gcggcacctc ccgcgagggc gggcagacag 1680
cccctggcag caccgcctc ttccaggtcc gcgccaacag cgctggagcc acccggtctg 1740
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cctcagccgc ctacctgtgg gtgggtacag gagccagcga ggcagagaag acggggggccc 1860
aggagctgct caggggtgctg cgggccccac ctgtgcaggt ggcagaaggc agcgagccag 1920
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acaagaagat ggatgccccat cctcctcgcc tctttgcctg ctccaacaag attggacgtt 2040
ttgtgatcga agaggttcct ggtgagctca tgcaggaaga cctggcaacg gatgacgtca 2100
tgcttctgga cacctgggac caggtctttg tctgggttg aaaggattct caagaagaag 2160
aaaagacaga agccttgact tctgctaagc ggtacatcga gacggaccca gccaatcggg 2220
atcgcgcgac gcccatcacc gtggtgaagc aaggctttga gcctccctcc tttgtgggt 2280
ggttccttgg ctgggatgat gattactggt ctgtggaccc cttggacagg gccatggctg 2340
agctggctgc ctgaggaggg gcagggccca cccatgtcac cggtcagtgc cttttggaac 2400
tgctcttccc tcaaagaggc cttagagcga gcagagcagc tctgctatga gtgtgtgtgt 2460
gtgtgtgtgt tgtttctttt ttttttttt acagtatcca aaaatagccc tgcaaaaatt 2520
cagagtcctt gcaaaattgt ctaaaatgtc agtgtttggg aaattaaatc caataaaaaa 2580
attttgaagt gtgaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2640
aaaaaaaaaa aaaaaaaaaa aaa 2663

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<210> 46

<211> 1441

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 46

```

Met Ser Gly Leu Gly Asp Ser Ser Ser Asp Pro Ala Asn Pro Asp Ser
 1          5          10          15
His Lys Arg Lys Gly Ser Pro Cys Asp Thr Leu Ala Ser Ser Thr Glu
 20          25          30
Lys Arg Arg Arg Glu Gln Glu Asn Lys Tyr Leu Glu Glu Leu Ala Glu
 35          40          45
Leu Leu Ser Ala Asn Ile Ser Asp Ile Asp Ser Leu Ser Val Lys Pro
 50          55          60
Asp Lys Cys Lys Ile Leu Lys Lys Thr Val Asp Gln Ile Gln Leu Met
 65          70          75          80
Lys Arg Met Glu Gln Glu Lys Ser Thr Thr Asp Asp Asp Val Gln Lys
 85          90          95
Ser Asp Ile Ser Ser Ser Ser Gln Gly Val Ile Glu Lys Glu Ser Leu
100          105          110

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Gly	Pro	Leu	Leu	Leu	Glu	Ala	Leu	Asp	Gly	Phe	Phe	Phe	Val	Val	Asn
		115					120					125			
Cys	Glu	Gly	Arg	Ile	Val	Phe	Val	Ser	Glu	Asn	Val	Thr	Ser	Tyr	Leu
	130					135					140				
Gly	Tyr	Asn	Gln	Glu	Glu	Leu	Met	Asn	Thr	Ser	Val	Tyr	Ser	Ile	Leu
145				150						155					160
His	Val	Gly	Asp	His	Ala	Glu	Phe	Val	Lys	Asn	Leu	Leu	Pro	Lys	Ser
			165						170					175	
Leu	Val	Asn	Gly	Val	Pro	Trp	Pro	Gln	Glu	Ala	Thr	Arg	Arg	Asn	Ser
			180					185					190		
His	Thr	Phe	Asn	Cys	Arg	Met	Leu	Ile	His	Pro	Pro	Asp	Glu	Pro	Gly
		195					200					205			
Thr	Glu	Asn	Gln	Glu	Ala	Cys	Gln	Arg	Tyr	Glu	Val	Met	Gln	Cys	Phe
	210					215					220				
Thr	Val	Ser	Gln	Pro	Lys	Ser	Ile	Gln	Glu	Asp	Gly	Glu	Asp	Phe	Gln
225				230						235					240
Ser	Cys	Leu	Ile	Cys	Ile	Ala	Arg	Arg	Leu	Pro	Arg	Pro	Pro	Ala	Ile
				245					250					255	
Thr	Gly	Val	Glu	Ser	Phe	Met	Thr	Lys	Gln	Asp	Thr	Thr	Gly	Lys	Ile
			260					265					270		
Ile	Ser	Ile	Asp	Thr	Ser	Ser	Leu	Arg	Ala	Ala	Gly	Arg	Thr	Gly	Trp
			275				280					285			
Glu	Asp	Leu	Val	Arg	Lys	Cys	Ile	Tyr	Ala	Phe	Phe	Gln	Pro	Gln	Gly
	290					295					300				
Arg	Glu	Pro	Ser	Tyr	Ala	Arg	Gln	Leu	Phe	Gln	Glu	Val	Met	Thr	Arg
305					310					315					320
Gly	Thr	Ala	Ser	Ser	Pro	Ser	Tyr	Arg	Phe	Ile	Leu	Asn	Asp	Gly	Thr
				325					330					335	
Met	Leu	Ser	Ala	His	Thr	Lys	Cys	Lys	Leu	Cys	Tyr	Pro	Gln	Ser	Pro
			340					345					350		
Asp	Met	Gln	Pro	Phe	Ile	Met	Gly	Ile	His	Ile	Ile	Asp	Arg	Glu	His
		355					360					365			
Ser	Gly	Leu	Ser	Pro	Gln	Asp	Asp	Thr	Asn	Ser	Gly	Met	Ser	Ile	Pro
	370				375						380				
Arg	Val	Asn	Pro	Ser	Val	Asn	Pro	Ser	Ile	Ser	Pro	Ala	His	Gly	Val
385					390					395					400
Ala	Arg	Ser	Ser	Thr	Leu	Pro	Pro	Ser	Asn	Ser	Asn	Met	Val	Ser	Thr
				405					410					415	
Arg	Ile	Asn	Arg	Gln	Gln	Ser	Ser	Asp	Leu	His	Ser	Ser	Ser	His	Ser
			420					425					430		
Asn	Ser	Ser	Asn	Ser	Gln	Gly	Ser	Phe	Gly	Cys	Ser	Pro	Gly	Ser	Gln
		435					440					445			
Ile	Val	Ala	Asn	Val	Ala	Leu	Asn	Lys	Gly	Gln	Ala	Ser	Ser	Gln	Ser
	450					455					460				
Ser	Lys	Pro	Ser	Leu	Asn	Leu	Asn	Asn	Pro	Pro	Met	Glu	Gly	Thr	Gly
465				470					475						480
Ile	Ser	Leu	Ala	Gln	Phe	Met	Ser	Pro	Arg	Arg	Gln	Val	Thr	Ser	Gly
				485					490					495	
Leu	Ala	Thr	Arg	Pro	Arg	Met	Pro	Asn	Asn	Ser	Phe	Pro	Pro	Asn	Ile
			500					505					510		
Ser	Thr	Leu	Ser	Ser	Pro	Val	Gly	Met	Thr	Ser	Ser	Ala	Cys	Asn	Asn
		515					520					525			
Asn	Asn	Arg	Ser	Tyr	Ser	Asn	Ile	Pro	Val	Thr	Ser	Leu	Gln	Gly	Met
	530					535					540				
Asn	Glu	Gly	Pro	Asn	Asn	Ser	Val	Gly	Phe	Ser	Ala	Ser	Ser	Pro	Val
545				550					555						560
Leu	Arg	Gln	Met	Ser	Ser	Gln	Asn	Ser	Pro	Ser	Arg	Leu	Asn	Ile	Gln
				565					570					575	
Pro	Ala	Lys	Ala	Glu	Ser	Lys	Asp	Asn	Lys	Glu	Ile	Ala	Ser	Thr	Leu
			580					585					590		

Asn	Glu	Met	Ile	Gln	Ser	Asp	Asn	Ser	Ser	Ser	Asp	Gly	Lys	Pro	Leu	595	600	605
Asp	Ser	Gly	Leu	Leu	His	Asn	Asn	Asp	Arg	Leu	Ser	Asp	Gly	Asp	Ser	610	615	620
Lys	Tyr	Ser	Gln	Thr	Ser	His	Lys	Leu	Val	Gln	Leu	Leu	Thr	Thr	Thr	625	630	635
Ala	Glu	Gln	Gln	Leu	Arg	His	Ala	Asp	Ile	Asp	Thr	Ser	Cys	Lys	Asp	645	650	655
Val	Leu	Ser	Cys	Thr	Gly	Thr	Ser	Asn	Ser	Ala	Ser	Ala	Asn	Ser	Ser	660	665	670
Gly	Gly	Ser	Cys	Pro	Ser	Ser	His	Ser	Ser	Leu	Thr	Ala	Arg	His	Lys	675	680	685
Ile	Leu	His	Arg	Leu	Leu	Gln	Glu	Gly	Ser	Pro	Ser	Asp	Ile	Thr	Thr	690	695	700
Leu	Ser	Val	Glu	Pro	Asp	Lys	Lys	Asp	Ser	Ala	Ser	Thr	Ser	Val	Ser	705	710	715
Val	Thr	Gly	Gln	Val	Gln	Gly	Asn	Ser	Ser	Ile	Lys	Leu	Glu	Leu	Asp	725	730	735
Ala	Ser	Lys	Lys	Lys	Glu	Ser	Lys	Asp	His	Gln	Leu	Leu	Arg	Tyr	Leu	740	745	750
Leu	Asp	Lys	Asp	Glu	Lys	Asp	Leu	Arg	Ser	Thr	Pro	Asn	Leu	Ser	Leu	755	760	765
Asp	Asp	Val	Lys	Val	Lys	Val	Glu	Lys	Lys	Glu	Gln	Met	Asp	Pro	Cys	770	775	780
Asn	Thr	Asn	Pro	Thr	Pro	Met	Thr	Lys	Pro	Thr	Pro	Glu	Glu	Ile	Lys	785	790	795
Leu	Glu	Ala	Gln	Ser	Gln	Phe	Thr	Ala	Asp	Leu	Asp	Gln	Phe	Asp	Gln	805	810	815
Leu	Leu	Pro	Thr	Leu	Glu	Lys	Ala	Ala	Gln	Leu	Pro	Gly	Leu	Cys	Glu	820	825	830
Thr	Asp	Arg	Met	Asp	Gly	Ala	Val	Thr	Ser	Val	Thr	Ile	Lys	Ser	Glu	835	840	845
Ile	Leu	Pro	Ala	Ser	Leu	Gln	Ser	Ala	Thr	Ala	Arg	Pro	Thr	Ser	Arg	850	855	860
Leu	Asn	Arg	Leu	Pro	Glu	Leu	Glu	Leu	Glu	Ala	Ile	Asp	Asn	Gln	Phe	865	870	875
Gly	Gln	Pro	Gly	Thr	Gly	Asp	Gln	Ile	Pro	Trp	Thr	Asn	Asn	Thr	Val	885	890	895
Thr	Ala	Ile	Asn	Gln	Ser	Lys	Ser	Glu	Asp	Gln	Cys	Ile	Ser	Ser	Gln	900	905	910
Leu	Asp	Glu	Leu	Leu	Cys	Pro	Pro	Thr	Thr	Val	Glu	Gly	Arg	Asn	Asp	915	920	925
Glu	Lys	Ala	Leu	Leu	Glu	Gln	Leu	Val	Ser	Phe	Leu	Ser	Gly	Lys	Asp	930	935	940
Glu	Thr	Glu	Leu	Ala	Glu	Leu	Asp	Arg	Ala	Leu	Gly	Ile	Asp	Lys	Leu	945	950	955
Val	Gln	Gly	Gly	Gly	Leu	Asp	Val	Leu	Ser	Glu	Arg	Phe	Pro	Pro	Gln	965	970	975
Gln	Ala	Thr	Pro	Pro	Leu	Ile	Met	Glu	Glu	Arg	Pro	Asn	Leu	Tyr	Ser	980	985	990
Gln	Pro	Tyr	Ser	Ser	Pro	Phe	Pro	Thr	Ala	Asn	Leu	Pro	Ser	Pro	Phe	995	1000	1005
Gln	Gly	Met	Val	Arg	Gln	Lys	Pro	Ser	Leu	Gly	Thr	Met	Pro	Val	Gln	1010	1015	1020
Val	Thr	Pro	Pro	Arg	Gly	Ala	Phe	Ser	Pro	Gly	Met	Gly	Met	Gln	Pro	1025	1030	1035
Arg	Gln	Thr	Leu	Asn	Arg	Pro	Pro	Ala	Ala	Pro	Asn	Gln	Leu	Arg	Leu	1045	1050	1055
Gln	Leu	Gln	Gln	Arg	Leu	Gln	Gly	Gln	Gln	Gln	Leu	Ile	His	Gln	Asn	1060	1065	1070

Arg Gln Ala Ile Leu Asn Gln Phe Ala Ala Thr Ala Pro Val Gly Ile  
 1075 1080 1085  
 Asn Met Arg Ser Gly Met Gln Gln Gln Ile Thr Pro Gln Pro Pro Leu  
 1090 1095 1100  
 Asn Ala Gln Met Leu Ala Gln Arg Gln Arg Glu Leu Tyr Ser Gln Gln  
 1105 1110 1115 1120  
 His Arg Gln Arg Gln Leu Ile Gln Gln Gln Arg Ala Met Leu Met Arg  
 1125 1130 1135  
 Gln Gln Ser Phe Gly Asn Asn Leu Pro Pro Ser Ser Gly Leu Pro Val  
 1140 1145 1150  
 Gln Thr Gly Asn Pro Arg Leu Pro Gln Gly Ala Pro Gln Gln Phe Pro  
 1155 1160 1165  
 Tyr Pro Pro Asn Tyr Gly Thr Asn Pro Gly Thr Pro Pro Ala Ser Thr  
 1170 1175 1180  
 Ser Pro Phe Ser Gln Leu Ala Ala Asn Pro Glu Ala Ser Leu Ala Asn  
 1185 1190 1195 1200  
 Arg Asn Ser Met Val Ser Arg Gly Met Thr Gly Asn Ile Gly Gly Gln  
 1205 1210 1215  
 Phe Gly Thr Gly Ile Asn Pro Gln Met Gln Gln Asn Val Phe Gln Tyr  
 1220 1225 1230  
 Pro Gly Ala Gly Met Val Pro Gln Gly Glu Ala Asn Phe Ala Pro Ser  
 1235 1240 1245  
 Leu Ser Pro Gly Ser Ser Met Val Pro Met Pro Ile Pro Pro Pro Gln  
 1250 1255 1260  
 Ser Ser Leu Leu Gln Gln Thr Pro Pro Ala Ser Gly Tyr Gln Ser Pro  
 1265 1270 1275 1280  
 Asp Met Lys Ala Trp Gln Gln Gly Ala Ile Gly Asn Asn Asn Val Phe  
 1285 1290 1295  
 Ser Gln Ala Val Gln Asn Gln Pro Thr Pro Ala Gln Pro Gly Val Tyr  
 1300 1305 1310  
 Asn Asn Met Ser Ile Thr Val Ser Met Ala Gly Gly Asn Thr Asn Val  
 1315 1320 1325  
 Gln Asn Met Asn Pro Met Met Ala Gln Met Gln Met Ser Ser Leu Gln  
 1330 1335 1340  
 Met Pro Gly Met Asn Thr Val Cys Pro Glu Gln Ile Asn Asp Pro Ala  
 1345 1350 1355 1360  
 Leu Arg His Thr Gly Leu Tyr Cys Asn Gln Leu Ser Ser Thr Asp Leu  
 1365 1370 1375  
 Leu Lys Thr Glu Ala Asp Gly Thr Gln Gln Val Gln Gln Val Gln Val  
 1380 1385 1390  
 Phe Ala Asp Val Gln Cys Thr Val Asn Leu Val Gly Gly Asp Pro Tyr  
 1395 1400 1405  
 Leu Asn Gln Pro Gly Pro Leu Gly Thr Gln Lys Pro Thr Ser Gly Pro  
 1410 1415 1420  
 Gln Thr Pro Gln Ala Gln Gln Lys Ser Leu Arg Gln Gln Leu Leu Thr  
 1425 1430 1435 1440  
 Glu

&lt;210&gt; 47

&lt;211&gt; 4547

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
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&lt;400&gt; 47

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60  
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